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PATENT
Attorney Docket 061834-5032

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: **Vernon ALVAREZ** *et al.*

Patent No. 7,053,177

Issued: May 30, 2006

Application No. 09/079,678

Filed: May 15, 1998

For: **RANDOM PEPTIDES THAT BIND TO GASTRO-
INTESTINAL TRACT (GIT) TRANSPORT
RECEPTORS AND RELATED METHODS**

Group Art Unit: 1654

Examiner: Roy Teller

Certificate

AUG 02 2006

of Correction

REQUEST FOR CERTIFICATE OF CORRECTION UNDER 37 C.F.R. 1.322

This is a request for the issuance of a Certificate of Correction under 37 C.F.R. 1.322 in the above-referenced patent to correct an Office mistake. Two (2) copies of form PTO-1050 are enclosed. The complete Certificate of Correction involves one hundred fifty-nine (159) pages.

The requested correction is the inclusion of sequence identifiers 31 to 407 in the sequence listing located at the end of the specification. Applicants submitted a substitute sequence listing on May 3, 2000 which contained sequence identifiers 1 to 407. However, the letters patent only contained sequence identifiers 1 to 30. The sequence listing containing all 407 sequence identifiers had been assigned sequence name US09079678 by the Patent Office and was accessible on PAIR. The error omitting sequence identifiers 31 to 407 from the letters patent thus clearly was made by the Office and correction under 37 C.F.R. 1.322 is requested. As the errors identified in the above-referenced U.S. Patent occurred through the fault of the U.S. Patent Office, no fee is enclosed. However, if there are any additional fees due in connection with the filing of this Request, the Commissioner is hereby authorized to charge any fees due to Deposit Account No. 50-0310.

Dated: July 31, 2006
Morgan, Lewis & Bockius LLP
Customer No. 09629
1111 Pennsylvania Avenue, N.W.
Washington, D.C. 20004
Tel. No.: 202-739-3000

Respectfully submitted
Morgan, Lewis & Bockius LLP

Christopher J. Betti
Christopher J. Betti, Ph.D.
Registration No. 56,890

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. 7,053,177
 ISSUED: May 30, 2006
 INVENTORS: Vernon L. Alvarez *et al.*

Page 1 of 159

It is hereby certified that errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

At the end of the sequence listing below column 103, please insert the following sequence identifiers and sequences.

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Arg	Trp	Pro	Ser	Val	Gly	Tyr	Lys	Gly	Asn	Gly	Ser	Asp	Thr	Ile	Asp
1		5		10		15									
Val	His	Ser	Asn	Asp	Ala	Ser	Thr	Lys	Arg	Ser	Leu	Ile	Tyr	Asn	His
	20		25		30										
Arg	Arg	Pro	Leu	Phe	Pro										
	35														

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Arg	Thr	Phe	Glu	Asn	Asp	Gly	Leu	Gly	Val	Gly	Arg	Ser	Ile	Gln	Lys
1		5		10		15									
Lys	Ser	Asp	Arg	Trp	Tyr	Ala	Ser	His	Asn	Ile	Arg	Ser	His	Phe	Ala
	20		25		30										
Ser	Met	Ser	Pro	Ala	Gly	Lys									
	35														

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly His Thr Asp Ser
1 5 10 15
Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu
20 25 30
Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys
1 5 10 15
Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu
20 25 30
Pro Ser Asp Gln Gly Pro Pro
35

(2) INFORMATION FOR SEQ ID NO: 35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser
1 5 10 15
Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg
20 25 30
Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 36:
(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr
 1 5 10 15
 Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala
 20 25 30
 His Asn Asn Arg Ala Leu Ala
 35

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Arg Ser Ile Thr Asp Gly Gly Ile Asn Glu Val Asp Leu Ser Ser Val
 1 5 10 15
 Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His
 20 25 30
 Arg Pro Thr Leu Lys Arg Pro
 35

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly
 1 5 10 15
 Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro
 20 25 30
 Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala
1 5 10 15
Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser
20 25 30
Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser
35 40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly
1 5 10 15
Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg
20 25 30
Asp Asn Thr Asn Arg Asn Ala
35

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp
1 5 10 15
Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Ile Arg Ala Arg
20 25 30
Pro Gln Asn Arg Asp Arg Gln
35

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids
(B) TYPE: amino acid

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(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser
1 5 10 15
Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr
20 25 30
His Ala Pro His Arg Pro
35

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30
Pro Arg Gly Arg Arg His Pro
35

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly
1 5 10 15
Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys
20 25 30
His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
35 40

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala
1 5 10 15
Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys
20 25 30
His Lys Pro Leu Arg Arg Pro
35

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn
1 5 10 15
Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr
20 25 30
Pro Ser Asn Arg Gly His Lys
35

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp
1 5 10 15
Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg
20 25 30
Val Leu Lys Ala Pro Leu Pro
35

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp

1 5 10 15

Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn

20 25 30

His Ala His Pro Ser His Gly Ala Val Ala Lys Ile

35 40

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His

1 5 10 15

Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro

20 25 30

Ala Asn Ser Gly Asp Pro Asn

35

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp

1 5 10 15

Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro

20 25 30

Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys

35 40

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
 1 5 10 15
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
 20 25 30
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
 1 5 10 15
 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
 20 25 30
 Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly
 1 5 10 15
 Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr
 20 25 30
 Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

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Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu
 1 5 10 15
 Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp
 20 25 30
 Pro Pro Val Ser Thr Pro
 35

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
 1 5 10 15
 Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
 20 25 30
 Arg Thr Arg Ser Arg Pro Asn
 35

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TCTCACTCCT CGAGATCCGG CGCTTATGAG AGTCCGGATG GTCGGGGGGG
 TCGGAGCTAT 60
 GTGGGGGGCG GGGGTGGNTG TGGTAACATT GGTCGGAAGC ATAACCTGTG
 GGGGCTGCGT 120
 ACCGCGTCGC CGGCCTGCTG GGA CTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
 177

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

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Patent No. 7,053,177

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TCTCACTCCT CGAGTCCTCG CTCCTTCTGG CCCGTTGTGT CCCGGCATGA
GTCGTTTGGG 60
ATCTCTAACT ATTTGGGNTG TGGTTATCGT ACATGTATCT CCGGCACGAT
GACTAAGTCT 120
AGCCCGATTT ACCCTCGGCA TTCGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TCTCACTCCT CGAGTAGTAG CTCCGATTGG GGTGGTGTGC CTGGGAAGGT
GGTTAGGGAG 60
CGCTTTAAGG GGC GCGGTTG TGGTATTTC ATCACCTCCG TGCTCACTGG
GAAGCCCAAT 120
CCGTGTCCGG AGCCTAAGGC GGCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TCTCACTCCT CGAGAGTTGG CCAGTGCACG GATTCTGATG TGCGGCGTCC
TTGGGCCAGG 60
TCTTGCGCTC ATCAGGGTTG TGGTGCGGGC ACTCGCAACT CGCACGGCTG
CATCACCCGT 120
CCTCTCCGCC AGGCTAGCGC TCATTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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Patent No. 7,053,177

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TCTCACTCCT CGAGCCACTC CGGTGGTATG AATAGGGCCT ACGGGGATGT
GTTTAGGGAG 60
CTTCGTGATC GGTGGAACGC CACTTCCCAC CACTCTGCC CCACCCCTCA
GCTCCCCCGT 120
GGGCCTAATT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TCTCACTCCT CGAGTCCGTG CGGGGGGTCG TGGGGGCGTT TTATGCAGGG
TGGCCTTTTC 60
GGCGGTAGGA CTGATGGTTG TGGTGCCCAT AGAAACCGCA CTTCTGCGTC
GTTAGAGCCC 120
CCGAGCAGCG ACTACTCTAG AATCGAAGGT CGCGCTAGAC CTTCGAGA 168

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCTCACTCCT CGAGGGGCGC CGCCGATCAG CGGCGGGGGT GGTCCGAGAA
CTTGGGGTTG 60
CCTAGGGTGG GGTGGGACGC CATCGCTCAC AATAGCTATA CGTTCACCTC
GCGCCGCCCCG 120
CGCCCCCCT CTAGA 135

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TCTCACTCCT CGAGCGGTGG GGAGGTCAGC TCCTGGGGCC GCGTGAATGA
CCTCTGCGCT 60
AGGGTGAGTT GGACTGGTTG TGGTACTGCT CGTTCGCGC GTACCGACAA
CAAAGGCTTT 120

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Patent No. 7,053,177

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CTTCCTAAGC ACTCGTCACT CCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TCTCACTCCT CGAGTGATAG TGACGGGGAT CATTATGGGC TTCGGGGGGG
GGTGCGTTGT 60
TCGCTTCGTG ATAGGGGTTG TGGTCTGGCC CTGTCCACCG TCCATGCTGG
TCCCCCTCT 120
TTTACCCCA AGCTCTCCAG CCCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TCTCACTCCT CGAGGAGCTT GGGTAATTAT GCGTCACCG GGA CTGTGGA
CGTGACGGTT 60
TTGCCCATGC CTGGCCACGC CAACCACCTT GGTGTCTCCT CCGCCTCTAG
CTCTGATCCT 120
CCGCGGCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TCTCACTCCT CGAGAACTAC GACGGCTAAG GGGTGTCTTC TCGGAAGCTT
CGGCGTTCTT 60
AGTGGGTGCT CATTTACGCC AACCTCTCCA CCGCCCCACC TAGGATACCC
CCCCACTCC 120
GTCAATTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCTCACTCCT CGAGCCCGAA GTTGTCCAGC GTGGGTGTTA TGAATAAGGT
CACGGAGCTG 60

CCCACGGAGG GGCCTAACGC CATTAGTATT CCGATCTCCG CGACCCTCGG
CCCGCGCAAC 120

CCGCTCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAG CTGTGCAACT CGGTGACTAA
GAAGTTTCGC 60

CCGGGCTGGC GGGATCACGC CAATCCCTCC ACCCATCATC GTACTCCCCC
GCCAGCCAG 120

TCCAGCCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAT GACCCGTGTG GTGCCAGTCG
TTGGCGGGGG 60

GGCAACAGCT TGTTTGTTG TGGTCTTCGT TGTAAGTGGG CGCAGAGCAC
CCCGAGTGGC 120

AGGATCCATT CCACTTCGAC CAGCTCTAGA ATCGAAGGTG CGCTAGACCT TCGAGA
176

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs

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Patent No. 7,053,177

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:
TCTCACTCCT CGAGTAAGTC CGGGGAGGGG GGTGACAGTA GCAGGGGCGA
GACGGGCTGG 60
GCGAGGGTTC GGTCTCACGC CATGACTGCT GGCCGCTTTC GGTGGTACAA
CCAGTTGCC 120
TCTGATCGGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:
TCTCACTCCT CGAGGTCGAG CGCCAATAAT TGCGAGTGGA AGTCTGATTG
GATGCGCAGG 60
GCCTGTATTG CTCGTTACGC CAACAGTTCG GGCCCCGCCC GCGCCGTCGA
CACTAAGGCC 120
GCGCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO: 72:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:
TCTCACTCCT CGAGTAAGTG GTCGTGGAGT TCGAGGTGGG GCTCCCCGCA
GGATAAGGTT 60
GAGAAGACCA GGGCGGGTTG TGGTGGTAGT CCCAGCAGCA CCAATTGTCA
CCCCTACACC 120
TTTGCCCCC CCCC GCAAGC CGGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 73:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Patent No. 7,053,177

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCTCACTCCT CGAGTGGGTT CTGGGAGTTT AGCAGGGGGC TTTGGGATGG
GGAGAACCGT 60
AAGAGTGTCC GGTCGGGTTG TGGTTTTTCGT GGCTCCTCTG CTCAGGGCCC
GTGTCCGGTC 120
ACGCCTGCCA CCATTGACAA ACACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCTCACTCCT CGAGTGAGAG CGGGCGGTGC CGTAGCGTGA GCCGGTGGAT
GACGACGTGG 60
CAGACGCAGA AGGGCGGTTG TGGTTCCAAT GTTCCCGCG GTTCGCCCCCT
CGACCCCTCT 120
CACCAGACCG GGCATGCCAC TACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TCTCACTCCT CGAGGGAGTG GAGGTTTGCC GGGCCGCCGT TGGACCTGTG
GGCGGGTCCG 60
AGCTTGCCCT CTTTAAACGC CAGTTCCAC CCTCGCGCCC TGCGCACCTA
TTGGTCCAG 120
CGGCCCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

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Patent No. 7,053,177

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TCTCACTCCT CGAGGATGGA GGACATCAAG AACTCGGGGT GGAGGGACTC
TTGTAGGTGG 60
GGTGACCTGA GGCCTGGTTG TGGTAGCCGC CAGTGGTACC CCTCGAATAT
GCGTTCTAGC 120
AGAGATTACC CCGCGGGGGG CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCTCACTCCT CGAGTCATCC GTGGTACAGG CATTGGAACC ATGGTGACTT
CTCTGGTTTCG 60
GGCCAGTCAC GCCACACCCC GCCGGAGAGC CCCCACCCCG GCCGCCCTAA
TGCCACCATT 120
TCTAGAATCG AAGGTCGCGC TAGACCTTCG AG 152

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TCTCACTCCT CGAGATATAA GCACGATATC GGTTCGATG CTGGGGTTGA
CAAGAAGTCG 60
TCGTCTGTGC GTGGTGGTTG TGGTGCTCAT TNGTCGCCAC CCCGCGCCGG
CCGTGGTCCT 120
CGCGGCACGA TGGTTAGCAG GCTTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCTCACTCCT CGAGTCAGGG CTCCAAGCAG TGTATGCAGT ACCGCACCGG
TCGTTTGACG 60

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Patent No. 7,053,177

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GTGGGGTCTG AGTATGGTTG TGGTATGAAC CCCGCCCCGCC ATGCCACGCC
CGCTTATCCG 120
GCGCGCCTGC TGCCACGCTA TCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TCTCACTCCT CGAGTGGGCG GACTACTAGT GAGATTTCTG GGCTCTGGGG
TTGGGGTGAC 60
GACCGGAGCG GTTATGGTTG GGGTAACACG CTCCGCCCCA ACTACATCCC
TTATAGGCAG 120
GCGACGAACA GGCATCGTTA TACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCTCACTCCT CGAGGTGGAA TTGGACTGTC TTGCCCCGCCA CTGGCGGGCA
TTACTGGACG 60
CGTTTCGACGG ACTATCACGC CATTAACAAT CACAGGCCGA GCATCCCCCA
CCAGCATCCG 120
ACCCCTATCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TCTCACTCCT CGAGTTGGTC GTCGTGGAAT TGGAGCTCTA AGACTACTCG
TCTGGGCGAC 60
AGGGCGACTC GGGAGGGTTG TGGTCCCAGC CAGTCTGATG GCTGTCCTTA
TAACGGCCGC 120

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Patent No. 7,053,177

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CTTACGACCG TCAAGCCTCG CACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TCTCACTCCT CGAGTGGTAG TTTGAACGCA TGGCAACCGC GGTCATGGGT
GGGGGGCGCG 60
TTCCGGTCAC ACGCCAACAA TAACTTGAAC CCAAGCCCA CCATGGTTAC
TNGTCACCCT 120
ACCTCTAGAA TCGAAGGTCG CGCTAGACCT TCGAGA 156

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

TCTCACTCCT CGAGGTATTC GGGTTTGTCC CCGCGGGACA ACGGTCCCGC
TTGTAGTCAG 60
GAGGCTACCT TGGAGGGTTG TGGTGCGCAG AGGCTGATGT CCACCCGTCG
CAAGGGCCGC 120
AACTCCCGCC CCGGGTGGAC GCTCTCTAGA ATCGAAGGTC GCGCTAGACC CTTCGAGA
178

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCTCACTCCT CGAGCGTGGG GAATGATAAG ACTAGCAGGC CGGTTTCCTT
CTACGGGCGC 60
GTTAGTGATC TGTGGAACGC CAGCTTGATG CCGAAGCGTA CTCCCAGCTC
GAAGCGCCAC 120
GATGATGGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

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Patent No. 7,053,177

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(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TCTCACTCCT CGAGTACTCC CCCAGTAGG GAGGCGTATA GTAGGCCCTA
TAGTGTCGAT 60
AGCGATTTCGG ATACGAACGC CAAGCACAGC TCCCACAACC GCCGTNTGCG
GACGCGCAGC 120
CGCCCGAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TCTCACTCCT CGAGATGGCC TAGTGTTGGT TACAAGGGTA ATGGCAGTGA
CACTATTGAT 60
GTTACAGCA ATGACGCCAG TACTAAGAGG TCCCTCATCT ATAACCACCG
CCGCCCCNTC 120
TTTCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TCTCACTCCT CGAGAACGTT TGAGAACGAC GGGCTGGGCG TCGGCCGGTC
TATTCAGAAG 60
AAGTCGGATA GGTGGTACGC CAGCCACAAC ATTCGTAGCC ATTCGCGTC
CATGTCTCCC 120
GCTGGTAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid

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Patent No. 7,053,177

MORGAN, LEWIS & BOCKIUS LLP
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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:
TCTCACTCCT CGAGCTATTG TCGGGTTAAG GGTGGTGGGG AGGGGGGGCA
TACGGATTCC 60
AATCTGGCTA GGTCGGGTTG TGGTAAGGTG GCCAGGACCA GCAGGCTTCA
GCATATCAAC 120
CCGCGCGCTA CCCCCCCTC CCGGTCTAGA ATCGAAGGTC 160

(2) INFORMATION FOR SEQ ID NO: 90:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:
TCTCACTCCT CGAGTTGGAC TCGGTGGGGC AAGCACANTC ATGGGGGGTT
TGTGAACAAG 60
TCTCCCCCTG GGAAGAACGC CACGAGCCCC TACACCGACG CCCAGCTGCC
CAGTGATCAG 120
GGTCCTCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 91:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:
TCTCACTCCT CGAGTCAGGT TGATTCGTTT CGTAATAGCT TTCGGTGGTA
TGAGCCGAGC 60
AGGGCTCTGT GCCATGGTTG TGGTAAGCGC GACACCTCCA CCACTCGTAT
CCACAATAGC 120
CCCAGCGACT CCTATCCTAC ACGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 92:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
TCTCACTCCT CGAGCTTTTT GCGGTTCCAG AGTCCGAGGT TCGAGGATTA
CAGTAGGACG 60
ATCTNTCGGT TGC GCAACGC CACGAACCCG AGTAATGTCT CCGATGCGCA
CAATAACCGG 120
GCCTTGGCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:
TCTCACTCCT CGAGGAGCAT CACCGACGGG GGCATCAATG AGGTGGACCT
GAGTAGTGTG 60
TCGAACGTTC TTGAGAACGC CAACTCGCAT AGGGCCTACA GGAAGCATCG
CCCGACCTTG 120
AAGCGTCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:
TCTCACTCCT CGAGTTCGAA GGTGAGCAGC CCGAGGGGATC CGACGGTCCC
GCGGAAGGGC 60
GGCAATGTTG ATTATGGTTG TGGTCACAGG TCTTCCGCCC GGATGCCTAC
CTCCGCTCTG 120
TCGTGATCA CGAAGTGCTA CACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
TCTCACTCCT CGAGAGCCAG TANGCAGGGC GGCCGGGGTG TTGCCCCTGA
GTTTGGGGCG 60

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Patent No. 7,053,177

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AGCGTTTTGG GTNGTGGTTG TGGTAGCGCC ACTTATTACA CGAACTCCAC
CAGCTGCAAG 120
GATGCTATGG GCCACAATA CTCGTCTAGA ATCGAAGGTC GCGNTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

TCTCACTCCT CGAGATGGTG CGAGAAGCAC AAGTTTACGG CTGCGCGTTG
CAGCGCGGGG 60
GCGGGTTTTG AGAGGGANGC CAGCCGTCCG CCCCAGCCTG CCCACCGGGA
TAATACCAAC 120
CGTAATGCNT NTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCTCACTCCT CGAGTTTTCA GGTGTACCCG GACCATGGTC TGGAGAGGCA
TGCTTTGGAC 60
GGGACGGGTC CGCTTTACGC CATGCCCCGGC CGCTGGATTA GGGCGCGTCC
GCAGAACAGG 120
GACCGCCAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCTCACTCCT CGAGCAGGTG TACGGACAAC GAGCAGTGCC CCGATACCGG
GANTAGGTCT 60
CGTTCCGTTA GTAACGCCAG GTACTTTTCG AGCAGGTTGC TCAAGACTCA
CGCCCCCAT 120
CGCCCTTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

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Patent No. 7,053,177

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(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TCTCACTCCT CGAGTGCCAG GGATAGCGGG CCTGCGGAGG ATGGGTCCCG
CGCCGTCCGG 60
TTGAACGGGG TTGAGAACGC CAACACTAGG AAGTCCTCCC GCAGTAACCC
GCGGGGTAGG 120
CGCCATCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TCTCACTCCT CGAGTTCCGC CGATGCGGAG AAGTGTGCGG GCAGTCTGTT
GTGGTGGGGT 60
AGGCAGAACA ACTCCGGTTG TGGTTCGCCC ACGAAGAAGC ATCTGAAGCA
CCGCAATCGC 120
AGTCAGACCT CCTCTTCGTC CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TCTCACTCCT CGAGACCGAA GAACGTGGCC GATGCTTATT CGTCTCAGGA
CGGGGCGGCG 60
GCCGAGGAGA CGTCTCACGC CAGTAATGCC GCGCGGAAGT CCCCTAAGCA
CAAGCCCTTG 120
AGGCGGCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

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Patent No. 7,053,177

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(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:
TCTCACTCCT CGAGAGGCAG TACGGGGACG GCCGGCGGCG AGCGTTCCGG
GGTGCTCAAC 60
CTGCACACCA GGGATAACGC CAGCGGCAGC GGTTCAAAC CGTGGTACCC
TTCGAATCGG 120
GGTCACAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 103:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:
TCTCACTCCT CGAGGTGGGG GTGGGAGAGG AGTCCGTCCG ACTACGATTC
TGATATGGAC 60
TTGGGGGCGA GGAGGTACGC CACCCGCACC CACCGCGCGC CCCCTCGCGT
CTTGAAGGCT 120
CCCCTGCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 104:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:
TCTCACTCCT CGAGGCACTG GAAGTGCAGG GGCTCTCAGG CTGCCTACGG
GGACAAGGAT 60
ATCGGGAGGT CCAGGGGTTG TGGTTCCATT ACAAAGAATA AACTAATCA
CGCCCATCCT 120
AGCCACGGCG CCGTTGCTAA GATCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:
TCTCACTCCT CGAGCCGCGA GGAGGCGAAC TGGGACGGCT ATAAGAGGGA
GATGAGCCAC 60
CGGAGTCGCT TTTGGGACGC CACCCACCTG TCCCGCCCTC GCCGCCCCGC
TAACTCTGGT 120
GACCCTAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
TCTCACTCNT CGAGAGAGTT CGCGGAGAGG AGGTTGTGGG GGTGTGATGA
CCTGAGTTGG 60
CGTCTCGACG CGGAGGGTTG TGGTCCCCT CCGAGCAATC GGGCCGTCAA
GCATCGCAAG 120
CCCCGCCCCAC GCTCCCCCGC ACTCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
TCTCACTCNT NGAGTGATCA CGCGTTGGGG ACGAATCTGA GGTCTGACAA
TGCCAAGGAG 60
CCGGGTGATT ACAACTGTTG TGGTAACGGG AACTCTACCG GGCGAAAGGT
TTTAAACCGT 120
AGGCGCCCCT CCGCCATCCC CANTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
 TCTCACTCCT CGAGGCATAT TTCTGAGTAT AGCTTTGCGA ATTCCCACTT
 GATGGGTGGC 60
 GAGTCCAAGC GGAAGGGTTG TGGTATTAAC GGCTCCTTTT CTCCCACTTG
 TCCCCGCTCC 120
 CCCACCCCAG CCTTCCGCCG CACCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
 177

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TCTCACTCCT CGAGCCGGGA GAGCGGGATG TGGGGTAGTT GGTGGCGTGG
 TCACAGGTTG 60
 AATTCCACGG GGGGTAACGC CAACATGAAT GCTAGTCTGC CCCCCGACCC
 CCCTGTTTCC 120
 ACTCCGTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAG 158

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
 1 5 10 15
 Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
 20 25 30
 Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
 35 40 45
 Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
 50 55 60
 Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
 65 70 75 80
 Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
 85 90 95
 Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
 100 105 110
 Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
 115 120 125

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Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
 130 135 140
 Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
 145 150 155 160
 Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
 165 170 175
 Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His
 180 185 190
 Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
 195 200 205
 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
 210 215 220
 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
 225 230 235 240
 Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
 245 250 255
 Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
 260 265 270
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
 275 280 285
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
 290 295 300
 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
 305 310 315 320
 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
 325 330 335
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
 340 345 350
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
 355 360 365
 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
 370 375 380
 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu
 385 390 395 400
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val
 405 410 415
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val
 420 425 430
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr
 435 440 445
 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val
 450 455 460
 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys
 465 470 475 480
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu
 485 490 495

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Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser
 500 505 510
 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe
 515 520 525
 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn
 530 535 540
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg
 545 550 555 560
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala
 565 570 575
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr
 580 585 590
 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser
 595 600 605
 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu
 610 615 620
 Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly
 625 630 635 640
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu
 645 650 655
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr
 660 665 670
 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys
 675 680 685
 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser
 690 695 700
 Gln Lys Gln Met
 705

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

TCCGGACTCT CATAAGCGCC GG

22

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
ACAACGGGCC AGAAAGAGCG AG 22

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
ACACCACCCC AATCGGAGCT AC 22

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:
TCAGAATCCG TGCACTGGCC AA 22

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:
GCCCTATTCA TACCACCGGA GT 22

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:
CATCAGTCCT ACCGCCGAAA AG 22

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
CGTATAGCTA TTGTGAGCGA TG 22

(2) INFORMATION FOR SEQ ID NO: 118:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:
ACGCGCGGAA CGAGCAGTAC CA 22

(2) INFORMATION FOR SEQ ID NO: 119:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:
CCATAATGAT CCCCGTCACT AT 22

(2) INFORMATION FOR SEQ ID NO: 120:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:
AGACACCCCT TAGCCGTCGT AG 22

(2) INFORMATION FOR SEQ ID NO: 121:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:
AGCTCCGTGA CCTTAGTCAT AA 22

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGCACAGCTC AGCGCCGCAC CA

22

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGGGTCATC AGCGCCGCAC CA

22

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGTCACCCCC CTCCCCGGAC TT

22

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ACTCGCAATT ATTGGCGCTC GA

22

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
GTCTTCTCAA CCTTATCCTG CG 22

(2) INFORMATION FOR SEQ ID NO: 127:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:
AAAGCCCCCT GCTAAACTCC CA 22

(2) INFORMATION FOR SEQ ID NO: 128:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:
CTGCGTCTGC CACGTCGTCA TC 22

(2) INFORMATION FOR SEQ ID NO: 129:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:
GTTAAAAGAG GGCAAGCTCG GA 22

(2) INFORMATION FOR SEQ ID NO: 130:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:
CCGAGTTCTT GATGTCCTCC AT 22

(2) INFORMATION FOR SEQ ID NO: 131:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:
TCCAATGCCT GTACCACGGA TG 22

(2) INFORMATION FOR SEQ ID NO: 132:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:
TCGCAACCGA TATCGTGCTT AT 22

(2) INFORMATION FOR SEQ ID NO: 133:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:
TGCATACACT GCTTGGAGCC CT 22

(2) INFORMATION FOR SEQ ID NO: 134:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:
GAAATCTCAC TAGTAGTCCG CC 22

(2) INFORMATION FOR SEQ ID NO: 135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:
GCGGGCAAGA CAGTCCAATT CC 22

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
GAGCTCCAAT TCCACGACGA CC 22

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:
GGTTGCCATG CGTTCAAAC AC 22

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:
TCCCGCGGGG ACAAACCCGA AT 22

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:
CTGCTAGTCT TATCATTCCC CA 22

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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Patent No. 7,053,177

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:
CTATCGACAC TATAGGGCCT AC 22

(2) INFORMATION FOR SEQ ID NO: 141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:
TACCCTTGTA ACCCACTA GG 22

(2) INFORMATION FOR SEQ ID NO: 142:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:
TTCTTCTGAA TAGACCGGCC GA 22

(2) INFORMATION FOR SEQ ID NO: 143:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:
CCACCACCCT TAACCCGACA AT 22

(2) INFORMATION FOR SEQ ID NO: 144:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:
AGGGGGAGAC TTGTTCAAA AC 22

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- (2) INFORMATION FOR SEQ ID NO: 145:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:
 CGGCTCATAC CACCGAAAGC TA 22
- (2) INFORMATION FOR SEQ ID NO: 146:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:
 ATCGTCCTAC TGTAATCCTC GA 22
- (2) INFORMATION FOR SEQ ID NO: 147:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:
 GACACACTAC TCAGGTCCAC CT 22
- (2) INFORMATION FOR SEQ ID NO: 148:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:
 CCATAATCAA CATTGCCGCC CT 22
- (2) INFORMATION FOR SEQ ID NO: 149:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
CAAAACGCTC GCCCCAAACT CA 22

(2) INFORMATION FOR SEQ ID NO: 150:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:
GTAAACTTGT GCTTCTCGCA CC 22

(2) INFORMATION FOR SEQ ID NO: 151:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:
CCATGGTCCG GGTACACCTG AA 22

(2) INFORMATION FOR SEQ ID NO: 152:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:
GTTACTAACG GAACGAGACC TA 22

(2) INFORMATION FOR SEQ ID NO: 153:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:
TGTTGGCGTT CTCAACCCCG TT 22

(2) INFORMATION FOR SEQ ID NO: 154:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:
ACAACCGGAG TTGTTCTGCC TA 22

(2) INFORMATION FOR SEQ ID NO: 155:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:
TAAGCATCGG CCACGTTCTT CG 22

(2) INFORMATION FOR SEQ ID NO: 156:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:
TTATCCCTGG TGTGCAGGTT GA 22

(2) INFORMATION FOR SEQ ID NO: 157:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:
TATCAGAATC GTAGTCGGAC GG 22

(2) INFORMATION FOR SEQ ID NO: 158:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:
CTTTGTAATG GAACCACAAC CC 22

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:
CGGTGGCTCA TCTCCCTCTT AT 22

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
ATCAGACTGG CTGGGACCAC AA 22

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
CACAACTCC TCTCCGCGAA CT 22

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:
AGATTCGTCC CCAACGCGTG AT 22

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:
 GGGAATTCGC AAAGCTATAC TC 22

(2) INFORMATION FOR SEQ ID NO: 164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:
 CCCC GTGGAA TTCAACCTGT GA 22

(2) INFORMATION FOR SEQ ID NO: 165:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:
 GTCGTCTTTC CAGACGT 17

(2) INFORMATION FOR SEQ ID NO: 166:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
 CTTGCATGCC TGCAGGTCGA C 21

(2) INFORMATION FOR SEQ ID NO: 167:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
 Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala Phe Glu

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1 5 10 15
 Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln Leu Ser
 20 25 30
 Phe Thr Pro Glu Glu
 35

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
 1 5 10 15
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
 20 25 30
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe
 1 5 10 15
 Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro
 20 25 30
 Thr Pro Gln Leu Pro Arg Gly Pro Asn
 35 40

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
 1 5 10 15

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Ser Asp Ser Asp
20

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn
20 25

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Thr Asn Ala Lys His Ser Ser His Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:
 Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
 1 5 10 15
 Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
 20 25 30
 Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
 35 40 45
 Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
 50 55 60
 Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
 65 70 75 80
 Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
 85 90 95
 Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
 100 105 110
 Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
 115 120 125
 Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
 130 135 140
 Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
 145 150 155 160
 Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
 165 170 175
 Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His

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180 185 190
 Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
 195 200 205
 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
 210 215 220
 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
 225 230 235 240
 Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
 245 250 255
 Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
 260 265 270
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
 275 280 285
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
 290 295 300
 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
 305 310 315 320
 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
 325 330 335
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
 340 345 350
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
 355 360 365
 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
 370 375 380
 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu
 385 390 395 400
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val
 405 410 415
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val
 420 425 430
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr
 435 440 445
 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val
 450 455 460
 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys
 465 470 475 480
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu
 485 490 495
 Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser
 500 505 510
 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe
 515 520 525
 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn
 530 535 540
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg

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545 550 555 560
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala
 565 570 575
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr
 580 585 590
 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser
 595 600 605
 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu
 610 615 620
 Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly
 625 630 635 640
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu
 645 650 655
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr
 660 665 670
 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys
 675 680 685
 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser
 690 695 700
 Gln Lys Gln Met
 705

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 88...2583
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

GAATTCCGTC TCGACCACTG AATGGAAGAA AAGGACTTTT AACCACCATT
 TTGTGACTTA 60
 CAGAAAGGAA TTTGAATAAA GAAAACT ATG ATA CTT CAG GCC CAT CTT CAC TCC
 114

Met Ile Leu Gln Ala His Leu His Ser

1 5

CTG TGT CTT CTT ATG CTT TAT TTG GCA ACT GGA TAT GGC CAA GAG GGG 162

Leu Cys Leu Leu Met Leu Tyr Leu Ala Thr Gly Tyr Gly Gln Glu Gly

10 15 20 25
 AAG TTT AGT GGA CCC CTG AAA CCC ATG ACA TTT TCT ATT TAT GAA GGC 210

Lys Phe Ser Gly Pro Leu Lys Pro Met Thr Phe Ser Ile Tyr Glu Gly

30 35 40

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CAA GAA CCG AGT CAA ATT ATA TTC CAG TTT AAG GCC AAT CCT CCT GCT 258
Gln Glu Pro Ser Gln Ile Ile Phe Gln Phe Lys Ala Asn Pro Pro Ala
    45        50        55
GTG ACT TTT GAA CTA ACT GGG GAG ACA GAC AAC ATA TTT GTG ATA GAA 306
Val Thr Phe Glu Leu Thr Gly Glu Thr Asp Asn Ile Phe Val Ile Glu
    60        65        70
CGG GAG GGA CTT CTG TAT TAC AAC AGA GCC TTG GAC AGG GAA ACA AGA 354
Arg Glu Gly Leu Leu Tyr Tyr Asn Arg Ala Leu Asp Arg Glu Thr Arg
    75        80        85
TCT ACT CAC AAT CTC CAG GTT GCA GCC CTG GAC GCT AAT GGA ATT ATA 402
Ser Thr His Asn Leu Gln Val Ala Ala Leu Asp Ala Asn Gly Ile Ile
    90        95       100       105
GTG GAG GGT CCA GTC CCT ATC ACC ATA GAA GTG AAG GAC ATC AAC GAC 450
Val Glu Gly Pro Val Pro Ile Thr Ile Glu Val Lys Asp Ile Asn Asp
    110       115       120
AAT CGA CCC ACG TTT CTC CAG TCA AAG TAC GAA GGC TCA GTA AGG CAG 498
Asn Arg Pro Thr Phe Leu Gln Ser Lys Tyr Glu Gly Ser Val Arg Gln
    125       130       135
AAC TCT CGC CCA GGA AAG CCC TTC TTG TAT GTC AAT GCC ACA GAC CTG 546
Asn Ser Arg Pro Gly Lys Pro Phe Leu Tyr Val Asn Ala Thr Asp Leu
    140       145       150
GAT GAT CCG GCC ACT CCC AAT GGC CAG CTT TAT TAC CAG ATT GTC ATC 594
Asp Asp Pro Ala Thr Pro Asn Gly Gln Leu Tyr Tyr Gln Ile Val Ile
    155       160       165
CAG CTT CCC ATG ATC AAC AAT GTC ATG TAC TTT CAG ATC AAC AAC AAA 642
Gln Leu Pro Met Ile Asn Asn Val Met Tyr Phe Gln Ile Asn Asn Lys
    170       175       180       185
ACG GGA GCC ATC TCT CTT ACC CGA GAG GGA TCT CAG GAA TTG AAT CCT 690
Thr Gly Ala Ile Ser Leu Thr Arg Glu Gly Ser Gln Glu Leu Asn Pro
    190       195       200
GCT AAG AAT CCT TCC TAT AAT CTG GTG ATC TCA GTG AAG GAC ATG GGA 738
Ala Lys Asn Pro Ser Tyr Asn Leu Val Ile Ser Val Lys Asp Met Gly
    205       210       215
GGC CAG AGT GAG AAT TCC TTC AGT GAT ACC ACA TCT GTG GAT ATC ATA 786
Gly Gln Ser Glu Asn Ser Phe Ser Asp Thr Thr Ser Val Asp Ile Ile
    220       225       230
GTG ACA GAG AAT ATT TGG AAA GCA CCA AAA CCT GTG GAG ATG GTG GAA 834
Val Thr Glu Asn Ile Trp Lys Ala Pro Lys Pro Val Glu Met Val Glu
    235       240       245
AAC TCA ACT GAT CCT CAC CCC ATC AAA ATC ACT CAG GTG CGG TGG AAT 882
Asn Ser Thr Asp Pro His Pro Ile Lys Ile Thr Gln Val Arg Trp Asn
    250       255       260       265
GAT CCC GGT GCA CAA TAT TCC TTA GTT GAC AAA GAG AAG CTG CCA AGA 930
Asp Pro Gly Ala Gln Tyr Ser Leu Val Asp Lys Glu Lys Leu Pro Arg
    270       275       280
TTC CCA TTT TCA ATT GAC CAG GAA GGA GAT ATT TAC GTG ACT CAG CCC 978

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Phe Pro Phe Ser Ile Asp Gln Glu Gly Asp Ile Tyr Val Thr Gln Pro
 285 290 295
 TTG GAC CGA GAA GAA AAG GAT GCA TAT GTT TTT TAT GCA GTT GCA AAG 1026
 Leu Asp Arg Glu Glu Lys Asp Ala Tyr Val Phe Tyr Ala Val Ala Lys
 300 305 310
 GAT GAG TAC GGA AAA CCA CTT TCA TAT CCG CTG GAA ATT CAT GTA AAA 1074
 Asp Glu Tyr Gly Lys Pro Leu Ser Tyr Pro Leu Glu Ile His Val Lys
 315 320 325
 GTT AAA GAT ATT AAT GAT AAT CCA CCT ACA TGT CCG TCA CCA GTA ACC 1122
 Val Lys Asp Ile Asn Asp Asn Pro Pro Thr Cys Pro Ser Pro Val Thr
 330 335 340 345
 GTA TTT GAG GTC CAG GAG AAT GAA CGA CTG GGT AAC AGT ATC GGG ACC 1170
 Val Phe Glu Val Gln Glu Asn Glu Arg Leu Gly Asn Ser Ile Gly Thr
 350 355 360
 CTT ACT GCA CAT GAC AGG GAT GAA GAA AAT ACT GCC AAC AGT TTT CTA 1218
 Leu Thr Ala His Asp Arg Asp Glu Glu Asn Thr Ala Asn Ser Phe Leu
 365 370 375
 AAC TAC AGG ATT GTG GAG CAA ACT CCC AAA CTT CCC ATG GAT GGA CTC 1266
 Asn Tyr Arg Ile Val Glu Gln Thr Pro Lys Leu Pro Met Asp Gly Leu
 380 385 390
 TTC CTA ATC CAA ACC TAT GCT GGA ATG TTA CAG TTA GCT AAA CAG TCC 1314
 Phe Leu Ile Gln Thr Tyr Ala Gly Met Leu Gln Leu Ala Lys Gln Ser
 395 400 405
 TTG AAG AAG CAA GAT ACT CCT CAG TAC AAC TTA ACG ATA GAG GTG TCT 1362
 Leu Lys Lys Gln Asp Thr Pro Gln Tyr Asn Leu Thr Ile Glu Val Ser
 410 415 420 425
 GAC AAA GAT TTC AAG ACC CTT TGT TTT GTG CAA ATC AAC GTT ATT GAT 1410
 Asp Lys Asp Phe Lys Thr Leu Cys Phe Val Gln Ile Asn Val Ile Asp
 430 435 440
 ATC AAT GAT CAG ATC CCC ATC TTT GAA AAA TCA GAT TAT GGA AAC CTG 1458
 Ile Asn Asp Gln Ile Pro Ile Phe Glu Lys Ser Asp Tyr Gly Asn Leu
 445 450 455
 ACT CTT GCT GAA GAC ACA AAC ATT GGG TCC ACC ATC TTA ACC ATC CAG 1506
 Thr Leu Ala Glu Asp Thr Asn Ile Gly Ser Thr Ile Leu Thr Ile Gln
 460 465 470
 GCC ACT GAT GCT GAT GAG CCA TTT ACT GGG AGT TCT AAA ATT CTG TAT 1554
 Ala Thr Asp Ala Asp Glu Pro Phe Thr Gly Ser Ser Lys Ile Leu Tyr
 475 480 485
 CAT ATC ATA AAG GGA GAC AGT GAG GGA CGC CTG GGG GTT GAC ACA GAT 1602
 His Ile Ile Lys Gly Asp Ser Glu Gly Arg Leu Gly Val Asp Thr Asp
 490 495 500 505
 CCC CAT ACC AAC ACC GGA TAT GTC ATA ATT AAA AAG CCT CTT GAT TTT 1650
 Pro His Thr Asn Thr Gly Tyr Val Ile Ile Lys Lys Pro Leu Asp Phe
 510 515 520
 GAA ACA GCA GCT GTT TCC AAC ATT GTG TTC AAA GCA GAA AAT CCT GAG 1698
 Glu Thr Ala Ala Val Ser Asn Ile Val Phe Lys Ala Glu Asn Pro Glu

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525	530	535	
CCT CTA GTG TTT GGT GTG AAG TAC AAT GCA AGT TCT TTT GCC AAG TTC			1746
Pro Leu Val Phe Gly Val Lys Tyr Asn Ala Ser Ser Phe Ala Lys Phe			
540	545	550	
ACG CTT ATT GTG ACA GAT GTG AAT GAA GCA CCT CAA TTT TCC CAA CAC			1794
Thr Leu Ile Val Thr Asp Val Asn Glu Ala Pro Gln Phe Ser Gln His			
555	560	565	
GTA TTC CAA GCG AAA GTC AGT GAG GAT GTA GCT ATA GGC ACT AAA GTG			1842
Val Phe Gln Ala Lys Val Ser Glu Asp Val Ala Ile Gly Thr Lys Val			
570	575	580	585
GGC AAT GTG ACT GCC AAG GAT CCA GAA GGT CTG GAC ATA AGC TAT TCA			1890
Gly Asn Val Thr Ala Lys Asp Pro Glu Gly Leu Asp Ile Ser Tyr Ser			
590	595	600	
CTG AGG GGA GAC ACA AGA GGT TGG CTT AAA ATT GAC CAC GTG ACT GGT			1938
Leu Arg Gly Asp Thr Arg Gly Trp Leu Lys Ile Asp His Val Thr Gly			
605	610	615	
GAG ATC TTT AGT GTG GCT CCA TTG GAC AGA GAA GCC GGA AGT CCA TAT			1986
Glu Ile Phe Ser Val Ala Pro Leu Asp Arg Glu Ala Gly Ser Pro Tyr			
620	625	630	
CGG GTA CAA GTG GTG GCC ACA GAA GTA GGG GGG TCT TCC TTA AGC TCT			2034
Arg Val Gln Val Val Ala Thr Glu Val Gly Gly Ser Ser Leu Ser Ser			
635	640	645	
GTG TCA GAG TTC CAC CTG ATC CTT ATG GAT GTG AAT GAC AAC CCT CCC			2082
Val Ser Glu Phe His Leu Ile Leu Met Asp Val Asn Asp Asn Pro Pro			
650	655	660	665
AGG CTA GCC AAG GAC TAC ACG GGC TTG TTC TTC TGC CAT CCC CTC AGT			2130
Arg Leu Ala Lys Asp Tyr Thr Gly Leu Phe Phe Cys His Pro Leu Ser			
670	675	680	
GCA CCT GGA AGT CTC ATT TTC GAG GCT ACT GAT GAT GAT CAG CAC TTA			2178
Ala Pro Gly Ser Leu Ile Phe Glu Ala Thr Asp Asp Asp Gln His Leu			
685	690	695	
TTT CGG GGT CCC CAT TTT ACA TTT TCC CTC GGC AGT GGA AGC TTA CAA			2226
Phe Arg Gly Pro His Phe Thr Phe Ser Leu Gly Ser Gly Ser Leu Gln			
700	705	710	
AAC GAC TGG GAA GTT TCC AAA ATC AAT GGT ACT CAT GCC CGA CTG TCT			2274
Asn Asp Trp Glu Val Ser Lys Ile Asn Gly Thr His Ala Arg Leu Ser			
715	720	725	
ACC AGG CAC ACA GAC TTT GAG GAG AGG GCG TAT GTC GTC TTG ATC CGC			2322
Thr Arg His Thr Asp Phe Glu Glu Arg Ala Tyr Val Val Leu Ile Arg			
730	735	740	745
ATC AAT GAT GGG GGT CGG CCA CCC TTG GAA GGC ATT GTT TCT TTA CCA			2370
Ile Asn Asp Gly Gly Arg Pro Pro Leu Glu Gly Ile Val Ser Leu Pro			
750	755	760	
GTT ACA TTC TGC AGT TGT GTG GAA GGA AGT TGT TTC CGG CCA GCA GGT			2418
Val Thr Phe Cys Ser Cys Val Glu Gly Ser Cys Phe Arg Pro Ala Gly			
765	770	775	

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CAC CAG ACT GGG ATA CCC ACT GTG GGC ATG GCA GTT GGT ATA CTG CTG 2466
His Gln Thr Gly Ile Pro Thr Val Gly Met Ala Val Gly Ile Leu Leu
780 785 790
ACC ACC CTT CTG GTG ATT GGT ATA ATT TTA GCA GTT GTG TTT ATC CGC 2514
Thr Thr Leu Leu Val Ile Gly Ile Ile Leu Ala Val Val Phe Ile Arg
795 800 805
ATA AAG AAG GAT AAA GGC AAA GAT AAT GTT GAA AGT GCT CAA GCA TCT 2562
Ile Lys Lys Asp Lys Gly Lys Asp Asn Val Glu Ser Ala Gln Ala Ser
810 815 820 825
GAA GTC AAA CCT CTG AGA AGC TGAATTTGAA AAGGAATGTT TGAATTTATA TAGC
2617
Glu Val Lys Pro Leu Arg Ser
830
AAGTGCTATT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAACG
TGCATTATAA 2677
TTTTTTAAAC AGATATTCCC TCTTGTCCTT TAATATTTGC TAAATATTTT TTTTTTGAGG
2737
TGGAGTCTTG CTCTGTCGCC CAGGCTGGAG TACAGTGGTG TGATCCCAGC
TCACTGCAAC 2797
CTCCGCCTCC TGGGTTTACA TGATTCTCCT GCCTCAGCTT CCTAAGTAGC
TGGGTTTACA 2857
GGCACCCACC ACCATGCCCA GCTAATTTTT GTATTTTTAA TAGAGACGGG
GTTTCGCCAT 2917
TTGGCCAGGC TGGTCTTGAA CTCCTGACGT CAAGTGATCT GCCTGCCTTG
GTCTCCCAAT 2977
ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTTCA TGTGCTATAG
ACATTAGAGA 3037
GATTTTTCAT TTTTCCATGA CATTTTTCCT CTCTGCAAAT GGCTTAGCTA CTTGTGTTTT
3097
TCCCTTTTGG GGCAAGACAG ACTCATTAAT TATTCTGTAC ATTTTTTCTT
TATCAAGGAG 3157
ATATATCAGT GTTGTCTCAT AGAACTGCCT GGATTCCATT TATGTTTTTT CTGATTCCAT
3217
CCTGTGTCCC CTTATCCTT GACTCCTTTG GTATTTCACT GAATTTCAAA CATTTGTCAG
3277
AGAAGAAAAA AGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC
TTTTGCGGCC 3337
GCGAATTC 3345

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr
 1 5 10 15
 Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys
 20 25 30
 Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile
 35 40 45
 Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly
 50 55 60
 Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr
 65 70 75 80
 Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val
 85 90 95
 Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile
 100 105 110
 Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln
 115 120 125
 Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro
 130 135 140
 Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn
 145 150 155 160
 Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn
 165 170 175
 Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr
 180 185 190
 Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn
 195 200 205
 Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe
 210 215 220
 Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys
 225 230 235 240
 Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro
 245 250 255
 Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser
 260 265 270
 Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln
 275 280 285
 Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp
 290 295 300
 Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu
 305 310 315 320
 Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn
 325 330 335
 Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn
 340 345 350
 Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp

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355 360 365
 Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln
 370 375 380
 Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala
 385 390 395 400
 Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro
 405 410 415
 Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu
 420 425 430
 Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile
 435 440 445
 Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn
 450 455 460
 Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro
 465 470 475 480
 Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser
 485 490 495
 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr
 500 505 510
 Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn
 515 520 525
 Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys
 530 535 540
 Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val
 545 550 555 560
 Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser
 565 570 575
 Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp
 580 585 590
 Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly
 595 600 605
 Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro
 610 615 620
 Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr
 625 630 635 640
 Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile
 645 650 655
 Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr
 660 665 670
 Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe
 675 680 685
 Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr
 690 695 700
 Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys
 705 710 715 720
 Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Asp Phe Glu

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          725          730          735
Glu Arg Ala Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro
          740          745          750
Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val
          755          760          765
Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr
          770          775          780
Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly
          785          790          795          800
Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys
          805          810          815
Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser
          820          825          830

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1827 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

Met Ala Arg Lys Lys Phe Ser Gly Leu Glu Ile Ser Leu Ile Val Leu
 1           5           10          15
Phe Val Ile Val Thr Ile Ile Ala Ile Ala Leu Ile Val Val Leu Ala
 20          25          30
Thr Lys Thr Pro Ala Val Asp Glu Ile Ser Asp Ser Thr Ser Thr Pro
 35          40          45
Ala Thr Thr Arg Val Thr Thr Asn Pro Ser Asp Ser Gly Lys Cys Pro
 50          55          60
Asn Val Leu Asn Asp Pro Val Asn Val Arg Ile Asn Cys Ile Pro Glu
 65          70          75          80
Gln Phe Pro Thr Glu Gly Ile Cys Ala Gln Arg Gly Cys Cys Trp Arg
 85          90          95
Pro Trp Asn Asp Ser Leu Ile Pro Trp Cys Phe Phe Val Asp Asn His
100          105          110
Gly Tyr Asn Val Gln Asp Met Thr Thr Thr Ser Ile Gly Val Glu Ala
115          120          125
Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn
130          135          140
Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe
145          150          155          160
Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr
165          170          175
Val Lys Glu Phe Thr Gly Pro Thr Val Ser Asp Thr Leu Tyr Asp Val
180          185          190

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Lys Val Ala Gln Asn Pro Phe Ser Ile Gln Val Ile Arg Lys Ser Asn
 195 200 205
 Gly Lys Thr Leu Phe Asp Thr Ser Ile Gly Pro Leu Val Tyr Ser Asp
 210 215 220
 Gln Tyr Leu Gln Ile Ser Ala Arg Leu Pro Ser Asp Tyr Ile Tyr Gly
 225 230 235 240
 Ile Gly Glu Gln Val His Lys Arg Phe Arg His Asp Leu Ser Trp Lys
 245 250 255
 Thr Trp Pro Ile Phe Thr Arg Asp Gln Leu Pro Gly Asp Asn Asn Asn
 260 265 270
 Asn Leu Tyr Gly His Gln Thr Phe Phe Met Cys Ile Glu Asp Thr Ser
 275 280 285
 Gly Lys Ser Phe Gly Val Phe Leu Met Asn Ser Asn Ala Met Glu Ile
 290 295 300
 Phe Ile Gln Pro Thr Pro Ile Val Thr Tyr Arg Val Thr Gly Gly Ile
 305 310 315 320
 Leu Asp Phe Tyr Ile Leu Leu Gly Asp Thr Pro Glu Gln Val Val Gln
 325 330 335
 Gln Tyr Gln Gln Leu Val Gly Leu Pro Ala Met Pro Ala Tyr Trp Asn
 340 345 350
 Leu Gly Phe Gln Leu Ser Arg Trp Asn Tyr Lys Ser Leu Asp Val Val
 355 360 365
 Lys Glu Val Val Arg Arg Asn Arg Glu Ala Gly Ile Pro Phe Asp Thr
 370 375 380
 Gln Val Thr Asp Ile Asp Tyr Met Glu Asp Lys Lys Asp Phe Thr Tyr
 385 390 395 400
 Asp Gln Val Ala Phe Asn Gly Leu Pro Gln Phe Val Gln Asp Leu His
 405 410 415
 Asp His Gly Gln Lys Tyr Val Ile Ile Leu Asp Pro Ala Ile Ser Ile
 420 425 430
 Gly Arg Arg Ala Asn Gly Thr Thr Tyr Ala Thr Tyr Glu Arg Gly Asn
 435 440 445
 Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile
 450 455 460
 Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro
 465 470 475 480
 Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu
 485 490 495
 Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe
 500 505 510
 Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro
 515 520 525
 Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile
 530 535 540
 Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser
 545 550 555 560

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Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys
 565 570 575
 Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala
 580 585 590
 Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser
 595 600 605
 Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu
 610 615 620
 Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu
 625 630 635 640
 Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr
 645 650 655
 Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro
 660 665 670
 Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr
 675 680 685
 Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr
 690 695 700
 Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu
 705 710 715 720
 Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp
 725 730 735
 Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr
 740 745 750
 Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly
 755 760 765
 Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala
 770 775 780
 Asp Lys Ile Gly Leu His Leu Arg Gly Gly Tyr Ile Ile Pro Ile Gln
 785 790 795 800
 Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu
 805 810 815
 Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp
 820 825 830
 Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu
 835 840 845
 Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His
 850 855 860
 Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile
 865 870 875 880
 Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn
 885 890 895
 Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln
 900 905 910
 Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser
 915 920 925

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Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr
 930 935 940
 Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys
 945 950 955 960
 Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe
 965 970 975
 Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser
 980 985 990
 Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile
 995 1000 1005
 Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys Tyr
 1010 1015 1020
 His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln Lys Lys
 1025 1030 1035 1040
 Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr Pro Ile Ser
 1045 1050 1055
 Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys Glu Asn Pro Phe
 1060 1065 1070
 Gly Ile Gln Ile Arg Arg Arg Ser Ser Gly Arg Val Ile Trp Asp Ser
 1075 1080 1085
 Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln Phe Ile Gln Ile Ser Thr
 1090 1095 1100
 Arg Leu Pro Ser Glu Tyr Ile Tyr Gly Phe Gly Glu Val Glu His Thr
 1105 1110 1115 1120
 Ala Phe Lys Arg Asp Leu Asn Trp Asn Thr Trp Gly Met Phe Thr Arg
 1125 1130 1135
 Asp Gln Pro Pro Gly Tyr Lys Leu Asn Ser Tyr Gly Phe His Pro Tyr
 1140 1145 1150
 Tyr Met Ala Leu Glu Glu Glu Gly Asn Ala His Gly Val Phe Leu Leu
 1155 1160 1165
 Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr
 1170 1175 1180
 Tyr Arg Thr Val Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro
 1185 1190 1195 1200
 Thr Pro Gln Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro
 1205 1210 1215
 Val Met Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly
 1220 1225 1230
 Tyr Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala
 1235 1240 1245
 Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met Glu
 1250 1255 1260
 Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu Pro Gln
 1265 1270 1275 1280
 Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile Ile Ile Leu
 1285 1290 1295

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Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr Pro Ala Phe Glu
 1300 1305 1310
 Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp Pro Asn Thr Asn Asp
 1315 1320 1325
 Ile Cys Trp Ala Lys Val Trp Pro Asp Leu Pro Asn Ile Thr Ile Asp
 1330 1335 1340
 Lys Thr Leu Thr Glu Asp Glu Ala Val Asn Ala Ser Arg Ala His Val
 1345 1350 1355 1360
 Ala Phe Pro Asp Phe Phe Arg Thr Ser Thr Ala Glu Trp Trp Ala Arg
 1365 1370 1375
 Glu Ile Val Asp Phe Tyr Asn Glu Lys Met Lys Phe Asp Gly Leu Trp
 1380 1385 1390
 Ile Asp Met Asn Glu Pro Ser Ser Phe Val Asn Gly Thr Thr Thr Asn
 1395 1400 1405
 Gln Cys Arg Asn Asp Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu
 1410 1415 1420
 Thr Lys Arg Thr Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala
 1425 1430 1435 1440
 Glu Gln Ile Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His
 1445 1450 1455
 Asn Leu Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln
 1460 1465 1470
 Lys Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro
 1475 1480 1485
 Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala Arg
 1490 1495 1500
 Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe Ser Leu
 1505 1510 1515 1520
 Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe Phe Asn Asn
 1525 1530 1535
 Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu Gly Ala Phe Tyr
 1540 1545 1550
 Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr Arg Arg Gln Asp Pro
 1555 1560 1565
 Ala Ser Trp Asn Glu Thr Phe Ala Glu Met Ser Arg Asn Ile Leu Asn
 1570 1575 1580
 Ile Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Gln Met His Glu Ile
 1585 1590 1595 1600
 His Ala Asn Gly Gly Thr Val Ile Arg Pro Leu Leu His Glu Phe Phe
 1605 1610 1615
 Asp Glu Lys Pro Thr Trp Asp Ile Phe Lys Gln Phe Leu Trp Gly Pro
 1620 1625 1630
 Ala Phe Met Val Thr Pro Val Leu Glu Pro Tyr Val Gln Thr Val Asn
 1635 1640 1645
 Ala Tyr Val Pro Asn Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp
 1650 1655 1660

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Ile Gly Val Arg Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr
 1665 1670 1675 1680
 Ile Asn Leu His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro
 1685 1690 1695
 Ala Gln Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val
 1700 1705 1710
 Ala Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp
 1715 1720 1725
 Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val Gln
 1730 1735 1740
 Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys Arg Gly
 1745 1750 1755 1760
 Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His Val Trp Gly
 1765 1770 1775
 Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr Tyr Asn Gly Asn
 1780 1785 1790
 Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr Asn Met Ile Leu Arg
 1795 1800 1805
 Ile Asp Leu Thr Thr His Asn Val Thr Leu Glu Glu Pro Ile Glu Ile
 1810 1815 1820
 Asn Trp Ser
 1825

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 45...2099
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GCCTTACTGC AGGAAGGCAC TCCGAAGACA TAAGTCGGTG AGAC ATG GCT GAA GAT
56

Met Ala Glu Asp

1

AAA AGC AAG AGA GAC TCC ATC GAG ATG AGT ATG AAG GGA TGC CAG ACA 104

Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys Gly Cys Gln Thr

5 10 15 20

AAC AAC GGG TTT GTC CAT AAT GAA GAC ATT CTG GAG CAG ACC CCG GAT 152

Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu Gln Thr Pro Asp

25 30 35

CCA GGC AGC TCA ACA GAC AAC CTG AAG CAC AGC ACC AGG GGC ATC CTT 200

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Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr Arg Gly Ile Leu
 40 45 50
 GGC TCC CAG GAG CCC GAC TTC AAG GGC GTC CAG CCC TAT GCG GGG ATG 248
 Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro Tyr Ala Gly Met
 55 60 65
 CCC AAG GAG GTG CTG TTC CAG TTC TCT GGC CAG GCC CGC TAC CGC ATA 296
 Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala Arg Tyr Arg Ile
 70 75 80
 CCT CGG GAG ATC CTC TTC TGG CTC ACA GTG GCT TCT GTG CTG GTG CTC 344
 Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser Val Leu Val Leu
 85 90 95 100
 ATC GCG GCC ACC ATA GCC ATC ATT GCC CTC TCT CCA AAG TGC CTA GAC 392
 Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro Lys Cys Leu Asp
 105 110 115
 TGG TGG CAG GAG GGG CCC ATG TAC CAG ATC TAC CCA AGG TCT TTC AAG 440
 Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro Arg Ser Phe Lys
 120 125 130
 GAC AGT AAC AAG GAT GGG AAC GGA GAT CTG AAA GGT ATT CAA GAT AAA 488
 Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly Ile Gln Asp Lys
 135 140 145
 CTG GAC TAC ATC ACA GCT TTA AAT ATA AAA ACT GTT TGG ATT ACT TCA 536
 Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val Trp Ile Thr Ser
 150 155 160
 TTT TAT AAA TCG TCC CTT AAA GAT TTC AGA TAT GGT GTT GAA GAT TTC 584
 Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly Val Glu Asp Phe
 165 170 175 180
 CGG GAA GTT GAT CCC ATT TTT GGA ACG ATG GAA GAT TTT GAG AAT CTG 632
 Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp Phe Glu Asn Leu
 185 190 195
 GTT GCA GCC ATA CAT GAT AAA GGT TTA AAA TTA ATC ATC GAT TTC ATA 680
 Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile Ile Asp Phe Ile
 200 205 210
 CCA AAC CAC ACG AGT GAT AAA CAT ATT TGG TTT CAA TTG AGT CGG ACA 728
 Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln Leu Ser Arg Thr
 215 220 225
 CGG ACA GGA AAA TAT ACT GAT TAT TAT ATC TGG CAT GAC TGT ACC CAT 776
 Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His Asp Cys Thr His
 230 235 240
 GAA AAT GGC AAA ACC ATT CCA CCC AAC AAC TGG TTA AGT GTG TAT GGA 824
 Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu Ser Val Tyr Gly
 245 250 255 260
 AAC TCC AGT TGG CAC TTT GAC GAA GTG CGA AAC CAA TGT TAT TTT CAT 872
 Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln Cys Tyr Phe His
 265 270 275
 CAG TTT ATG AAA GAG CAA CCT GAT TTA AAT TTC CGC AAT CCT GAT GTT 920
 Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg Asn Pro Asp Val

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      280      285      290
CAA GAA GAA ATA AAA GAA ATT TTA CGG TTC TGG CTC ACA AAG GGT GTT   968
Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu Thr Lys Gly Val
      295      300      305
GAT GGT TTT AGT TTG GAT GCT GTT AAA TTC CTC CTA GAA GCA AAG CAC   1016
Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu Glu Ala Lys His
      310      315      320
CTG AGA GAT GAG ATC CAA GTA AAT AAG ACC CAA ATC CCG GAC ACG GTC   1064
Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile Pro Asp Thr Val
      325      330      335      340
ACA CAA TAC TCG GAG CTG TAC CAT GAC TTC ACC ACC ACG CAG GTG GGA   1112
Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr Thr Gln Val Gly
      345      350      355
ATG CAC GAC ATT GTC CGC AGC TTC CGG CAG ACC ATG GAC CAA TAC AGC   1160
Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met Asp Gln Tyr Ser
      360      365      370
ACG GAG CCC GGC AGA TAC AGG TTC ATG GGG ACT GAA GCC TAT GCA GAG   1208
Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu Ala Tyr Ala Glu
      375      380      385
AGT ATT GAC AGG ACC GTG ATG TAC TAT GGA TTG CCA TTT ATC CAA GAA   1256
Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro Phe Ile Gln Glu
      390      395      400
GCT GAT TTT CCC TTC AAC AAT TAC CTC AGC ATG CTA GAC ACT GTT TCT   1304
Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu Asp Thr Val Ser
      405      410      415      420
GGG AAC AGC GTG TAT GAG GTT ATC ACA TCC TGG ATG GAA AAC ATG CCA   1352
Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met Glu Asn Met Pro
      425      430      435
GAA GGA AAA TGG CCT AAC TGG ATG ATT GGT GGA CCA GAC AGT TCA CGG   1400
Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro Asp Ser Ser Arg
      440      445      450
CTG ACT TCG CGT TTG GGG AAT CAG TAT GTC AAC GTG ATG AAC ATG CTT   1448
Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val Met Asn Met Leu
      455      460      465
CTT TTC ACA CTC CCT GGA ACT CCT ATA ACT TAC TAT GGA GAA GAA ATT   1496
Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr Gly Glu Glu Ile
      470      475      480
GGA ATG GGA AAT ATT GTA GCC GCA AAT CTC AAT GAA AGC TAT GAT ATT   1544
Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu Ser Tyr Asp Ile
      485      490      495      500
AAT ACC CTT CGC TCA AAG TCA CCA ATG CAG TGG GAC AAT AGT TCA AAT   1592
Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp Asn Ser Ser Asn
      505      510      515
GCT GGT TTT TCT GAA GCT AGT AAC ACC TGG TTA CCT ACC AAT TCA GAT   1640
Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro Thr Asn Ser Asp
      520      525      530

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TAC CAC ACT GTG AAT GTT GAT GTC CAA AAG ACT CAG CCC AGA TCG GCT 1688
 Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln Pro Arg Ser Ala
 535 540 545
 TTG AAG TTA TAT CAA GAT TTA AGT CTA CTT CAT GCC AAT GAG CTA CTC 1736
 Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala Asn Glu Leu Leu
 550 555 560
 CTC AAC AGG GGC TGG TTT TGC CAT TTG AGG AAT GAC AGC CAC TAT GTT 1784
 Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp Ser His Tyr Val
 565 570 575 580
 GTG TAC ACA AGA GAG CTG GAT GGC ATC GAC AGA ATC TTT ATC GTG GTT 1832
 Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile Phe Ile Val Val
 585 590 595
 CTG AAT TTT GGA GAA TCA ACA CTG TTA AAT CTA CAT AAT ATG ATT TCG 1880
 Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His Asn Met Ile Ser
 600 605 610
 GGC CTT CCC GCT AAA ATA AGA ATA AGG TTA AGT ACC AAT TCT GCC GAC 1928
 Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr Asn Ser Ala Asp
 615 620 625
 AAA GGC AGT AAA GTT GAT ACA AGT GGC ATT TTT CTG GAC AAG GGA GAG 1976
 Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu Asp Lys Gly Glu
 630 635 640
 GGA CTC ATC TTT GAA CAC AAC ACG AAG AAT CTC CTT CAT CGC CAA ACA 2024
 Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu His Arg Gln Thr
 645 650 655 660
 GCT TTC AGA GAT AGA TGC TTT GTT TCC AAT CGA GCA TGC TAT TCC AGT 2072
 Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala Cys Tyr Ser Ser
 665 670 675
 GTA CTG AAC ATA CTG TAT ACC TCG TGT TAGGCACCTT TATGAAGAGA TGAAGAC
 2126
 Val Leu Asn Ile Leu Tyr Thr Ser Cys
 680 685
 ACTGGCATT T CAGTGGGATT GTAAGCATT GTAATAGCTT CATGTACAGC
 ATGCTGCTT 2186
 GTGAACAATC ATTAATTCTT CGATATTCT GTAGCTTGAA TGTAACCGCT
 TTAAGAAAGG 2246
 TTCTCAAATG TTTTGAAAAA AATAAAATGT TTAAAGT 2284

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys

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1 5 10 15
 Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu
 20 25 30
 Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr
 35 40 45
 Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro
 50 55 60
 Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala
 65 70 75 80
 Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser
 85 90 95
 Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro
 100 105 110
 Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro
 115 120 125
 Arg Ser Phe Lys Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly
 130 135 140
 Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val
 145 150 155 160
 Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly
 165 170 175
 Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp
 180 185 190
 Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile
 195 200 205
 Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln
 210 215 220
 Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His
 225 230 235 240
 Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu
 245 250 255
 Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln
 260 265 270
 Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg
 275 280 285
 Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu
 290 295 300
 Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu
 305 310 315 320
 Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile
 325 330 335
 Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr
 340 345 350
 Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met
 355 360 365
 Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu

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370      375      380
Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro
385      390      395      400
Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu
      405      410      415
Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met
      420      425      430
Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro
      435      440      445
Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val
      450      455      460
Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr
465      470      475      480
Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu
      485      490      495
Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp
      500      505      510
Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro
      515      520      525
Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln
      530      535      540
Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala
545      550      555      560
Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp
      565      570      575
Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile
      580      585      590
Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His
      595      600      605
Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr
      610      615      620
Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu
625      630      635      640
Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu
      645      650      655
His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala
      660      665      670
Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys
      675      680      685

```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Leu Val Pro Arg Gly Ser Pro Gly Ile Pro Gly Ser Arg Val Gly Gln

1 5 10 15

Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His

20 25 30

Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg

35 40 45

Pro Leu Arg Gln Ala Ser

50

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg

1 5 10 15

Leu Asn Gly

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Asp Gly Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr

1 5 10 15

Arg Lys Ser Ser Arg

20

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg

1 5 10 15

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Arg His Pro

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Ser Arg Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His
1 5 10 15
Ser Ser His Asn Arg
20

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

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Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
 1 5 10 15
 Ser Ser Val Arg Gly Gly Cys Gly
 20

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly
 1 5 10 15
 Cys Gly Ala His Ser Ser Pro Pro Arg Ala
 20 25

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr
 1 5 10 15
 Met Val Ser Arg Leu
 20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Lys Lys Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala

1 5 10 15

Phe Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln

20 25 30

Leu Ser Phe Thr Pro Glu Glu

35

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly

1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Asn Pro Arg Gly Arg Arg His Pro

1 5

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Asn Ala Lys His Ser Ser His Asn

1 5

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:
 Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:
 Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:
 Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
 1 5 10 15
 Ser Cys Ala

(2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala
 1 5 10 15
 Gly Thr Arg Asn Ser
 20

(2) INFORMATION FOR SEQ ID NO: 201:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala

1 5 10 15

Ser Gln His

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp

1 5 10 15

Ser Asp Ser Asp Thr Met Ala Lys His Ser Ser His Asn Arg Arg Leu

20 25 30

Arg Thr Arg Ser Arg Pro Asn Gly

35 40

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Tyr Ser Lys Val

1

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Phe Pro His Leu

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1

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Tyr Arg Gly Val

1

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Tyr Gln Thr Ile

1

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Thr Glu Gln Phe

1

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Thr Glu Val Met

1

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(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Thr Ser Ala Phe

1

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Tyr Thr Arg Phe

1

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...714

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC 48

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1 5 10 15

ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG 96

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

20 25 30

TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG 144

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu

35 40 45

GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA 192

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

50 55 60

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TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC   240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65       70       75       80
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA   288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85       90       95
GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT   336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100      105      110
AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA   384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115      120      125
ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT   432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130      135      140
GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT   480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145      150      155      160
GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA   528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165      170      175
GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC   576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180      185      190
TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC   624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195      200      205
ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT   672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210      215      220
GGA TCC CCA GGA ATT CCC GGG TCG ACT CGA GCG GCC GCA TCG TGA     717
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser
225      230      235

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
20      25      30

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu

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      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
    100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
    115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
    145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
    165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
    180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
    195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Gln
    225      230      235      240
Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr Val Gly
    245      250      255
Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr Pro Ala
    260      265      270
Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
    275      280

```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85      90      95

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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asp
 225 230 235 240
 His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly
 245 250 255
 Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe
 260 265 270
 Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 275 280

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser

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      100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Pro
      225      230      235      240
Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe Gly Gly
      245      250      255
Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala Ser Leu
      260      265      270
Glu Pro Pro Ser Ser Asp Tyr
      275

```

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110

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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Gly
 225 230 235 240
 Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn Leu His
 245 250 255
 Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr Pro Ser
 260 265 270
 Asn Arg Gly His Lys
 275

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

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      115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
      225      230      235      240
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
      245      250      255
Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu
      260      265      270
Pro Arg Gly Pro Asn
      275

```

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
  20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
  35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
  50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
  65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
  85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
  100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
  115     120     125

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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
 225 230 235 240
 Ser Gly Gly Met Asn Arg Ala Tyr
 245

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu

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165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
 225 230 235 240
 Val Phe Arg Glu Leu Arg Asp Arg
 245

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn
 225 230 235 240
 Ala Thr Ser His His Thr Arg Pro
 245

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Pro
 225 230 235 240
 Gln Leu Pro Arg Gly Pro Asn

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245

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
 225 230 235 240
 Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
 245 250 255
 Arg Pro

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn
 225 230 235 240
 Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro
 245 250 255
 Asn

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1         5         10        15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20        25        30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35        40        45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50        55        60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65        70        75        80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85        90        95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100        105       110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115        120       125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130        135       140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145        150       155       160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165        170       175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180        185       190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195        200       205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210        215       220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
225        230       235       240
Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
245        250       255
Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
260        265

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

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```

1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50      55      60
Leu Thr Gln Ser Met Ala Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115     120     125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130     135     140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145     150     155     160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165     170     175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180     185     190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195     200     205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210     215     220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
225     230     235     240
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
245     250     255
Asp Arg Trp Asn Ala Thr Ser Ala Ala Thr Arg Pro Thr Pro Gln Leu
260     265     270
Pro Arg Gly Pro Asn
275

```

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1       5       10      15

```

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser Ala
 225 230 235 240
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
 245 250 255
 Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
 260 265 270
 Gly Arg Arg His Pro
 275

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

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20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala
 225 230 235 240
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
 245 250 255
 Gly

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Gly Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

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```

      50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
      100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115     120     125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130     135     140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145     150     155     160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165     170     175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180     185     190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195     200     205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210     215     220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Asp Gly
225     230     235     240
Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys
      245     250     255
Ser Ser Arg

```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
      50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu

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85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
 225 230 235 240
 Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
 245 250 255
 Pro

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

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```

      115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
      225      230      235      240
Ala Asn Thr Arg Lys Ser Ser Arg
      245

```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115     120     125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130     135     140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145     150     155     160

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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Lys
 225 230 235 240
 Ser Ser Arg Ser Asn Pro Arg Gly
 245

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala

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195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asn
 225 230 235 240
 Pro Arg Gly Arg Arg His Pro
 245

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Arg
 225 230 235 240

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Lys Ser Ser Arg Ser Asn Pro Arg Gly
245

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
225 230 235 240
Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
245 250 255
Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
260 265 270
Arg Ser Arg Pro Asn

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275

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
 225 230 235 240
 Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
 245 250 255
 Ser Asp

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Arg
 225 230 235 240
 Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser
 245 250 255
 His Asn Arg

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1         5         10        15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20        25        30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35        40        45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50        55        60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65        70        75        80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85        90        95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100       105       110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115       120       125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130       135       140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145       150       155       160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165       170       175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180       185       190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195       200       205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210       215       220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn
225       230       235       240
Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro
245       250       255
Asn

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1         5         10        15

```

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn
 225 230 235 240
 Ala Lys His Ser Ser His Asn
 245

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

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50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ser
 225 230 235 240
 His Asn Arg Arg Leu Arg Thr Arg
 245

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Arg
 225 230 235 240
 Leu Arg Thr Arg Ser Arg Pro Asn
 245

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn

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130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255
 Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile
 260 265 270
 Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 275 280

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255
 Ala

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Val Arg
 225 230 235 240
 Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr
 245 250 255
 Arg Asn Ser

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Thr
 225 230 235 240
 Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Gln
 245 250 255
 His

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
 225 230 235 240

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Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser
 245 250 255
 Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg
 260 265 270
 Gly Pro Arg Gly Thr Met Val Ser Arg Leu
 275 280

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
 225 230 235 240
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser

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245 250 255
Val Arg Gly Gly Cys Gly
260

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Cys
225 230 235 240
Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly Cys Gly
245 250 255
Ala His Ser Ser Pro Pro Arg Ala
260

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(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Ala
 225 230 235 240
 His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr Met Val
 245 250 255
 Ser Arg Leu

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:
Ser Gly Ser Pro Pro Cys Cys Cys Ser Trp Gly Arg Phe Met Gln Gly
1 5 10 15
Gly Leu Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg
20 25 30
Thr Ser Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
35 40

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
1 5 10 15
Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
20 25 30
Gln Leu Pro Arg Gly Pro Asn Ser
35 40

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15
Ser Arg Pro Asn Gly
20

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu

1 5 10 15

Arg Gln Ala Ser Ala His Gly

20

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

(B) LOCATION: 1

(D) OTHER INFORMATION: "Xaa=Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

(B) LOCATION: 2

(D) OTHER INFORMATION: "Xaa=Ser, Ala or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Asp Xaa Asp Xaa Arg Arg Xaa Xaa

1 5

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

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(B) LOCATION: 7

(D) OTHER INFORMATION: "Xaa=Ala or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser

1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asp Ser Asp Val Arg Arg Pro Trp

1 5

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Ala Asp Gln Arg Arg Gly Trp

1 5

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Asp Gly Arg Gly Gly Arg Ser Tyr

1 5

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Val Arg Ser

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1

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 2...2

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Cys Xaa Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys
 1 5 10 15
 Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val
 20 25 30
 Ser Leu Ser Lys Gln
 35

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Ac-Cys
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:
Xaa Leu Asn Gly Gly Val Lys Met Tyr Val Glu Ser Val Asp Arg Tyr
1 5 10 15
Val Cys

(2) INFORMATION FOR SEQ ID NO: 268:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Ac-Cys
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:
Xaa Leu Asn Gly Gly Val Lys Phe Ile Thr Cys Met Tyr Val Glu Ser
1 5 10 15
Val Asp Arg Tyr Val Cys
20

(2) INFORMATION FOR SEQ ID NO: 269:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 2...2
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:
Cys Xaa Arg Leu Asn Gly Gly Val Ser Met Tyr Val Glu Ser Val Asp
1 5 10 15
Arg Tyr Val Cys Arg
20

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(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val
1 5 10 15
Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser
20 25 30
Asn Pro Arg Gly Arg Arg His Pro
35 40

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Xaa Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp
1 5 10 15
Gly Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu
20 25 30
Lys His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
35 40 45

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Xaa Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser

1 5 10 15

Trp Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala

20 25 30

Val Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu

35 40 45

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Xaa Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe

1 5 10 15

Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro

20 25 30

Thr Pro Gln Leu Pro Arg Gly Pro Asn

35 40

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Xaa Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val

1 5 10 15

Phe Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg

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20 25 30
 Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
 35 40

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
 1 5 10 15
 Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
 20 25 30
 Pro Gln Leu Pro Arg Gly Pro Asn
 35 40

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
 1 5 10 15
 Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
 20 25 30
 Pro Gln Leu Pro Arg Gly Pro Asn Ser
 35 40

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:
Xaa Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu
1 5 10 15
Thr Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala
20 25 30
Thr Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO: 278:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:
Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His
20 25 30
Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
35 40 45

(2) INFORMATION FOR SEQ ID NO: 279:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

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Xaa Ser Gly Ser Gly Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg
 1 5 10 15
 Arg Pro Trp Ala Arg Ser Cys Ala
 20

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
 Arg Ser Cys Ala
 20

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Xaa Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val
 1 5 10 15
 Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
 20 25 30
 Leu Arg Thr Arg Ser Arg Pro Asn Gly
 35 40

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:
Xaa Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu
1 5 10 15
Asn Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp
20 25 30
Tyr Pro Ser Asn Arg Gly His Lys
35 40

(2) INFORMATION FOR SEQ ID NO: 283:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:
Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala
20

(2) INFORMATION FOR SEQ ID NO: 284:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:
Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala

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20

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
 1 5 10 15
 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
 20 25 30
 Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

Xaa Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu
 1 5 10 15
 Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser
 20 25 30
 Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Xaa Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys
1 5 10 15
Ser Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg
20 25 30
Ala Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val
1 5 10 15
Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser
20 25 30
Asn Pro Arg Gly Arg Arg His Pro Gly Gly
35 40

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

Xaa Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly
1 5 10 15

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Patent No. 7,053,177

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Trp Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp
 20 25 30
 Tyr Asn Gln Leu Pro Ser Asp Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Xaa Ser Glu Ala Asn Leu Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
 1 5 10 15
 Arg Arg Asn Ser Ser Thr Arg Pro Arg Thr Ser Pro Asn Ser Val His
 20 25 30
 Ala Arg Tyr Pro Ser Thr Asp His Asp
 35 40

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=biotin-S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Xaa Gly Ser Gly Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro
 1 5 10 15
 Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His
 20 25 30
 Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn Gly
 35 40

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:
 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
 Arg Ser Cys Ala His Gln Gly
 20

(2) INFORMATION FOR SEQ ID NO: 293:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:
 Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
 1 5 10 15
 Leu Arg Gln Ala Ser Ala His Gly
 20

(2) INFORMATION FOR SEQ ID NO: 294:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:
 Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
 1 5 10 15
 Arg Arg His Pro Gly

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20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15

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Gly

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Xaa	Thr	Asn	Ala	Lys	His	Ser	Ser	His	Asn	Arg	Arg	Leu	Arg	Thr	Arg
1		5		10					15						
Ser	Arg	Pro	Asn												
		20													

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Xaa	Thr	Asn	Ala	Lys	His	Ser	Ser	His	Asn	Arg	Arg	Leu	Arg	Thr	Arg
1		5		10					15						

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

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Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Xaa Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly
 1 5 10 15
 Ala Gly Thr Arg Asn Ser
 20

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Xaa Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

Xaa Ser Arg Ala Asn Thr Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
 1 5 10 15
 Arg Arg Asn Ser Ser Thr Glu Pro Arg Leu Ser Pro Asn Ser Val His
 20 25 30
 Ala Arg Tyr Pro Ser Thr Asp His Asp
 35 40

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:
Xaa Ser Asn Pro Arg Gly Arg Arg His Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:
Xaa Glu Asn Ala Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:
Xaa Ala Asn Thr Arg Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other

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(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:
Xaa Thr Arg Lys Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 310:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:
Xaa Arg Lys Ser Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:
Xaa Lys Ser Ser Arg Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 312:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:
Xaa Ser Ser Arg Ser Asn Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:
Xaa Arg Ser Asn Pro Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:
Xaa Ser Asn Pro Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Xaa Pro Arg Gly Arg Arg His

1

5

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Xaa Arg Arg His Pro Gly

1

5

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Xaa Lys Ser Ser Arg Gly Asn

1

5

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

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Xaa Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Xaa Thr Asn Ala Lys His Ser Ser His Asn

1 5 10

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn

1 5 10

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg

1 5

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

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Xaa Arg Arg Leu Arg Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
1 5 10 15
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Cys
20

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:
Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:
Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:
Xaa Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Xaa Asn Arg Arg Arg Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
20 25 30
Arg Thr Arg Ser Arg Pro Asn Gly
35 40

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
1 5 10 15
Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
20 25 30
Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
35 40

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Xaa Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys
1 5 10 15
Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe Asn Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
1 5 10 15
Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:
 Xaa Ala Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 340:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:
 Xaa Ser Ala His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 341:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:
 Xaa Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 342:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

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Patent No. 7,053,177

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- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:
 Xaa Ser Ser His Ala Arg Arg Leu Arg Thr Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 343:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:
 Xaa Ser Ser His Asn Ala Arg Leu Arg Thr Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 344:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 Xaa Ser Ser His Asn Arg Ala Leu Arg Thr Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 345:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Xaa Ser Ser His Asn Arg Arg Ala Arg Thr Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Xaa Ser Ser His Asn Arg Arg Leu Ala Thr Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Xaa Ser Ser His Asn Arg Arg Leu Arg Ala Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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Patent No. 7,053,177

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(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:
 Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Xaa Gly Arg Asn His Asp Val Val Ser Ser Asn Thr His Lys Ser Tyr
 1 5 10 15
 Arg Ser Pro Arg Ser Ala Ser Tyr Pro Arg Leu Ser Asn Asp Arg Thr
 20 25 30
 Asp Arg Thr Glu Pro Ala Pro Ser Ser
 35 40

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

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Patent No. 7,053,177

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Xaa Arg Asn Thr Arg Asn Lys Thr Ser Arg Leu Ser Ala Asn Pro His

1 5 10 15

Arg Ser His Arg

20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 20...20

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser

1 5 10 15

Arg Pro Asn Xaa

20

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 10...10

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Arg Arg Leu Arg Thr Arg Ser Arg Lys Xaa

1 5 10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

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Patent No. 7,053,177

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr
20

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Xaa Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn
1 5 10 15
Gly Asn Ser Thr Gly
20

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

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Patent No. 7,053,177

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:
 Xaa Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 358:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:
 Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 359:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:
 Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 360:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid

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Patent No. 7,053,177

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: MEMORY
 - (B) STRAIN: DISPLAY MEMORY
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Xaa	Asn	Cys	Cys	Gly	Asn	Gly	Asn	Ser	Thr	Gly
1	5				10					

- (2) INFORMATION FOR SEQ ID NO: 361:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Xaa	Lys	Thr	Arg	Lys	Ser	Ser	Arg	Ser	Asn	Pro	Arg	Gly	Arg	Arg	His
1	5				10				15						

 Pro Gly

- (2) INFORMATION FOR SEQ ID NO: 362:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Xaa	Lys	Thr	Arg	Lys	Ser	Ser	Arg	Ser	Asn	Pro	Arg	Gly	Arg	Arg	His
1	5				10				15						

 Pro Gly

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(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Cys Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Leu Arg Cys Arg
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Xaa Ala Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Xaa Thr Ala Ala Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

Xaa Thr Asn Gly Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 369:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:
 Xaa Thr Asn Ala Lys Ala Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 370:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:
 Xaa Thr Asn Ala Lys His Ala Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 371:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:
 Xaa Thr Asn Ala Lys His Ser Ala His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 372:
(i) SEQUENCE CHARACTERISTICS:

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Patent No. 7,053,177

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- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:
Xaa Thr Asn Ala Lys His Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:
Xaa Thr Asn Ala Lys His Ser Ser His Ala Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (B) LOCATION: 1...1
 - (D) OTHER INFORMATION: Xaa=Lys(dns)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Ala Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids

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Patent No. 7,053,177

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Ala Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Ala Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Ala Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid

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Patent No. 7,053,177

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
 1 5 10 15
 Arg

(2) INFORMATION FOR SEQ ID NO: 382:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:
 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 383:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:
 Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 384:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:
 Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 385:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 386:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 387:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

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Patent No. 7,053,177

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Xaa Ala Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Xaa Pro Ala Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Xaa Pro Gly Ala Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Xaa Pro Gly Asp Ala Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Xaa Pro Gly Asp Tyr Ala Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:
Xaa Pro Gly Asp Tyr Asn Ala Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:
Xaa Pro Gly Asp Tyr Asn Cys Ala Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:
Xaa Pro Gly Asp Tyr Asn Cys Cys Ala Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Ala Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Ala Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Ala Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:
Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ala Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Pro Gly Asp Tyr Asn Cys Gly Asn Cys Asn Ser Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15
Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
20 25 30
Pro Arg Gly Arg Arg His Pro Gly
35 40

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala
1 5 10 15
Ser Ala His

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:
Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala His
20

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
1 5 10 15
Leu Arg Gln Ala Ser Ala His
20

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**UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION**

PATENT NO. 7,053,177
ISSUED: May 30, 2006
INVENTORS: Vernon L. Alvarez *et al.*

Page 1 of 159

It is hereby certified that errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

At the end of the sequence listing below column 103, please insert the following sequence identifiers and sequences.

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Arg	Trp	Pro	Ser	Val	Gly	Tyr	Lys	Gly	Asn	Gly	Ser	Asp	Thr	Ile	Asp
1		5		10		15									
Val	His	Ser	Asn	Asp	Ala	Ser	Thr	Lys	Arg	Ser	Leu	Ile	Tyr	Asn	His
	20		25		30										
Arg	Arg	Pro	Leu	Phe	Pro										
	35														

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Arg	Thr	Phe	Glu	Asn	Asp	Gly	Leu	Gly	Val	Gly	Arg	Ser	Ile	Gln	Lys
1		5		10		15									
Lys	Ser	Asp	Arg	Trp	Tyr	Ala	Ser	His	Asn	Ile	Arg	Ser	His	Phe	Ala
	20		25		30										
Ser	Met	Ser	Pro	Ala	Gly	Lys									
	35														

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly His Thr Asp Ser
1 5 10 15
Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu
20 25 30
Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys
1 5 10 15
Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu
20 25 30
Pro Ser Asp Gln Gly Pro Pro
35

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser
1 5 10 15
Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg
20 25 30
Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 Ser Phe Leu Arg Phe Gln Ser Pro Arg Phe Glu Asp Tyr Ser Arg Thr
 1 5 10 15
 Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala
 20 25 30
 His Asn Asn Arg Ala Leu Ala
 35

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 Arg Ser Ile Thr Asp Gly Gly Ile Asn Glu Val Asp Leu Ser Ser Val
 1 5 10 15
 Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His
 20 25 30
 Arg Pro Thr Leu Lys Arg Pro
 35

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly
 1 5 10 15
 Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro
 20 25 30
 Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids

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Patent No. 7,053,177

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(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala
1 5 10 15
Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser
20 25 30
Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser
35 40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly
1 5 10 15
Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg
20 25 30
Asp Asn Thr Asn Arg Asn Ala
35

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp
1 5 10 15
Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Ile Arg Ala Arg
20 25 30
Pro Gln Asn Arg Asp Arg Gln
35

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids
(B) TYPE: amino acid

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Patent No. 7,053,177

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(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser
 1 5 10 15
 Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr
 20 25 30
 His Ala Pro His Arg Pro
 35

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
 1 5 10 15
 Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
 20 25 30
 Pro Arg Gly Arg Arg His Pro
 35

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly
 1 5 10 15
 Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys
 20 25 30
 His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
 35 40

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala
1 5 10 15
Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys
20 25 30
His Lys Pro Leu Arg Arg Pro
35

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn
1 5 10 15
Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr
20 25 30
Pro Ser Asn Arg Gly His Lys
35

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp
1 5 10 15
Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg
20 25 30
Val Leu Lys Ala Pro Leu Pro
35

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp
1 5 10 15
Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn
20 25 30
His Ala His Pro Ser His Gly Ala Val Ala Lys Ile
35 40

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His
1 5 10 15
Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro
20 25 30
Ala Asn Ser Gly Asp Pro Asn
35

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp
1 5 10 15
Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro
20 25 30
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys
35 40

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
 1 5 10 15
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
 20 25 30
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu
 1 5 10 15
 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
 20 25 30
 Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly
 1 5 10 15
 Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr
 20 25 30
 Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr
 35 40

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

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Patent No. 7,053,177

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Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu
 1 5 10 15
 Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp
 20 25 30
 Pro Pro Val Ser Thr Pro
 35

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
 1 5 10 15
 Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
 20 25 30
 Arg Thr Arg Ser Arg Pro Asn
 35

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TCTCACTCCT CGAGATCCGG CGCTTATGAG AGTCCGGATG GTCGGGGGGG
 TCGGAGCTAT 60
 GTGGGGGGCG GGGGTGGNTG TGGTAACATT GGTCGGAAGC ATAACCTGTG
 GGGGCTGCGT 120
 ACCGCGTCGC CGGCCTGCTG GGACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
 177

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

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Patent No. 7,053,177

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TCTCACTCCT CGAGTCCTCG CTCTTTCTGG CCCGTTGTGT CCCGGCATGA
GTCGTTTGGG 60
ATCTCTAACT ATTTGGGNTG TGGTTATCGT ACATGTATCT CCGGCACGAT
GACTAAGTCT 120
AGCCCGATTT ACCCTCGGCA TTCGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TCTCACTCCT CGAGTAGTAG CTCCGATTGG GGTGGTGTGC CTGGGAAGGT
GGTTAGGGAG 60
CGCTTTAAGG GGC GCGGTTG TGGTATTTC ATCACCTCCG TGCTCACTGG
GAAGCCCAAT 120
CCGTGTCCGG AGCCTAAGGC GGCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TCTCACTCCT CGAGAGTTGG CCAGTGCACG GATTCTGATG TGCGGCGTCC
TTGGGCCAGG 60
TCTTGCGCTC ATCAGGGTTG TGGTGCGGGC ACTCGCAACT CGCACGGCTG
CATCACCCGT 120
CCTCTCCGCC AGGCTAGCGC TCATTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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Patent No. 7,053,177

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TCTCACTCCT CGAGCCACTC CGGTGGTATG AATAGGGCCT ACGGGGATGT
GTTTAGGGAG 60
CTTCGTGATC GGTGGAACGC CACTTCCCAC CACTCGCC CCACCCCTCA
GCTCCCCCGT 120
GGGCCTAATT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TCTCACTCCT CGAGTCCGTG CGGGGGGTCG TGGGGGCGTT TTATGCAGGG
TGGCCTTTTC 60
GGCGGTAGGA CTGATGGTTG TGGTGCCCAT AGAAACCGCA CTTCTGCGTC
GTTAGAGCCC 120
CCGAGCAGCG ACTACTCTAG AATCGAAGGT CGCGCTAGAC CTTCGAGA 168

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCTCACTCCT CGAGGGGCGC CGCCGATCAG CGGCGGGGGT GGTCCGAGAA
CTTGGGGTTG 60
CCTAGGGTGG GGTGGGACGC CATCGCTCAC AATAGCTATA CGTTCACCTC
GCGCCGCCCCG 120
CGCCCCCCT CTAGA 135

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TCTCACTCCT CGAGCGGTGG GGAGGTCAGC TCCTGGGGCC GCGTGAATGA
CCTCTGCGCT 60
AGGGTGAGTT GGA CTGGTTG TGGTACTGCT CGTTCCGCGC GTACCGACAA
CAAAGGCTTT 120

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Patent No. 7,053,177

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CTTCCTAAGC ACTCGTCACT CCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TCTCACTCCT CGAGTGATAG TGACGGGGGAT CATTATGGGC TTCGGGGGGG
GGTGCGTTGT 60
TCGCTTCGTG ATAGGGGTTG TGGTCTGGCC CTGTCCACCG TCCATGCTGG
TCCCCCTCT 120
TTTACCCCA AGCTCTCCAG CCCCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TCTCACTCCT CGAGGAGCTT GGGTAATTAT GCGTCACCG GGA CTGTGGA
CGTGACGGTT 60
TTGCCATGC CTGGCCACGC CAACCACCTT GGTGTCTCCT CCGCCTCTAG
CTCTGATCCT 120
CCGCGGCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TCTCACTCCT CGAGAACTAC GACGGCTAAG GGGTGTCTTC TCGGAAGCTT
CGGCGTTCTT 60
AGTGGGTGCT CATTACGCC AACCTCTCCA CCGCCCCACC TAGGATACCC
CCCCACTCC 120
GTCAATTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

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Patent No. 7,053,177

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCTCACTCCT CGAGCCCGAA GTTGTCCAGC GTGGGTGTTA TGACTAAGGT
CACGGAGCTG 60
CCCACGGAGG GGCCTAACGC CATTAGTATT CCGATCTCCG CGACCCTCGG
CCCGCGCAAC 120
CCGCTCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAG CTGTGCAACT CGGTGACTAA
GAAGTTTCGC 60
CCGGGCTGGC GGGATCACGC CAATCCCTCC ACCCATCATC GTACTCCCCC
GCCAGCCAG 120
TCCAGCCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TCTCACTCCT CGAGGTGGTG CGGCGCTGAT GACCCGTGTG GTGCCAGTCG
TTGGCGGGGG 60
GGCAACAGCT TGTTTGTTG TGGTCTTCGT TGTAGTGCGG CGCAGAGCAC
CCCGAGTGGC 120
AGGATCCATT CCACTTCGAC CAGCTCTAGA ATCGAAGGTG CGCTAGACCT TCGAGA
176

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs

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Patent No. 7,053,177

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:
TCTCACTCCT CGAGTAAGTC CGGGGAGGGG GGTGACAGTA GCAGGGGCGA
GACGGGCTGG 60
GCGAGGGTTC GGTCTCACGC CATGACTGCT GGCCGCTTTC GGTGGTACAA
CCAGTTGCCC 120
TCTGATCGGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:
TCTCACTCCT CGAGGTCGAG CGCCAATAAT TGCGAGTGGA AGTCTGATTG
GATGCGCAGG 60
GCCTGTATTG CTCGTTACGC CAACAGTTCG GGCCCCGCCC GCGCCGTCGA
CACTAAGGCC 120
GCGCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO: 72:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:
TCTCACTCCT CGAGTAAGTG GTCGTGGAGT TCGAGGTGGG GCTCCCCGCA
GGATAAGGTT 60
GAGAAGACCA GGGCGGGTTG TGGTGGTAGT CCCAGCAGCA CCAATTGTCA
CCCCTACACC 120
TTTGCCCCCC CCCCACAAGC CGGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 73:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Patent No. 7,053,177

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCTCACTCCT CGAGTGGGTT CTGGGAGTTT AGCAGGGGGC TTTGGGATGG
GGAGAACCGT 60
AAGAGTGTCC GGTCGGGTTG TGGTTTTCGT GGCTCCTCTG CTCAGGGCCC
GTGTCCGGTC 120
ACGCCTGCCA CCATTGACAA AACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCTCACTCCT CGAGTGAGAG CGGGCGGTGC CGTAGCGTGA GCCGGTGGAT
GACGACGTGG 60
CAGACGCAGA AGGGCGGTTG TGGTTCCAAT GTTCCCGCG GTTCGCCCT
CGACCCCTCT 120
CACCAGACCG GGCATGCCAC TACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TCTCACTCCT CGAGGGAGTG GAGGTTTGCC GGGCCGCCGT TGGACCTGTG
GGCGGGTCCG 60
AGCTTGCCCT CTTTAAACGC CAGTCCCAC CCTCGCGCCC TGCACACCTA
TTGGTCCAG 120
CGGCCCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

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Patent No. 7,053,177

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TCTCACTCCT CGAGGATGGA GGACATCAAG AACTCGGGGT GGAGGGACTC
TTGTAGGTGG 60
GGTGACCTGA GGCCTGGTTG TGGTAGCCGC CAGTGGTACC CCTCGAATAT
GCGTTCTAGC 120
AGAGATTACC CCGCGGGGGG CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCTCACTCCT CGAGTCATCC GTGGTACAGG CATTGGAACC ATGGTGACTT
CTCTGGTTTCG 60
GGCCAGTCAC GCCACACCCC GCCGGAGAGC CCCCACCCCG GCCGCCCTAA
TGCCACCATT 120
TCTAGAATCG AAGGTCGCGC TAGACCTTCG AG 152

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TCTCACTCCT CGAGATATAA GCACGATATC GGTTCGATG CTGGGGTTGA
CAAGAAGTCG 60
TCGTCTGTGC GTGGTGGTTG TGGTGCTCAT TNGTCGCCAC CCCGCGCCGG
CCGTGGTCCT 120
CGCGGCACGA TGGTTAGCAG GCTTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCTCACTCCT CGAGTCAGGG CTCCAAGCAG TGTATGCAGT ACCGCACCGG
TCGTTTGACG 60

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Patent No. 7,053,177

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GTGGGGTCTG AGTATGGTTG TGGTATGAAC CCCGCCCGCC ATGCCACGCC
CGCTTATCCG 120
GCGCGCCTGC TGCCACGCTA TCGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TCTCACTCCT CGAGTGGGCG GACTACTAGT GAGATTTCTG GGCTCTGGGG
TTGGGGTGAC 60
GACCGGAGCG GTTATGGTTG GGGTAACACG CTCCGCCCCA ACTACATCCC
TTATAGGCAG 120
GCGACGAACA GGCATCGTTA TACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCTCACTCCT CGAGGTGGAA TTGGACTGTC TTGCCCGCCA CTGGCGGCCA
TTACTGGACG 60
CGTTCGACGG ACTATCACGC CATTAAACAAT CACAGGCCGA GCATCCCCCA
CCAGCATCCG 120
ACCCCTATCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TCTCACTCCT CGAGTTGGTC GTCGTGGAAT TGGAGCTCTA AGACTACTCG
TCTGGGCGAC 60
AGGGCGACTC GGGAGGGTTG TGGTCCCAGC CAGTCTGATG GCTGTCCTTA
TAACGGCCGC 120

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Patent No. 7,053,177

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CTTACGACCG TCAAGCCTCG CACGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TCTCACTCCT CGAGTGGTAG TTTGAACGCA TGGCAACCGC GGTCATGGGT
GGGGGGCGCG 60
TTCCGGTCAC ACGCCAACAA TAACTTGAAC CCAAGCCCA CCATGGTTAC
TNGTCACCCT 120
ACCTCTAGAA TCGAAGGTCG CGCTAGACCT TCGAGA 156

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

TCTCACTCCT CGAGGTATTC GGGTTTGTCC CCGCGGGACA ACGGTCCCGC
TTGTAGTCAG 60
GAGGCTACCT TGGAGGGTTG TGGTGCGCAG AGGCTGATGT CCACCCGTCG
CAAGGGCCGC 120
AACTCCCGCC CCGGGTGGAC GCTCTCTAGA ATCGAAGGTC GCGCTAGACC CTTCGAGA
178

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCTCACTCCT CGAGCGTGGG GAATGATAAG ACTAGCAGGC CGGTTTCCTT
CTACGGGCGC 60
GTTAGTGATC TGTGGAACGC CAGCTTGATG CCGAAGCGTA CTCCCAGCTC
GAAGCGCCAC 120
GATGATGGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

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Patent No. 7,053,177

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(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TCTCACTCCT CGAGTACTCC CCCAGTAGG GAGGCGTATA GTAGGCCCTA
TAGTGTTCGAT 60
AGCGATTTCGG ATACGAACGC CAAGCACAGC TCCCACAACC GCCGTNTGCG
GACGCGCAGC 120
CGCCCGAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TCTCACTCCT CGAGATGGCC TAGTGTGGGT TACAAGGGTA ATGGCAGTGA
CACTATTGAT 60
GTTACACAGCA ATGACGCCAG TACTAAGAGG TCCCTCATCT ATAACCACCG
CCGCCCCNTC 120
TTTCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TCTCACTCCT CGAGAACGTT TGAGAACGAC GGGCTGGGCG TCGGCCGGTC
TATTCAGAAG 60
AAGTCGGATA GGTGGTACGC CAGCCACAAC ATTCGTAGCC ATTCGCGTC
CATGTCTCCC 120
GCTGGTAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid

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Patent No. 7,053,177

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:
TCTCACTCCT CGAGCTATTG TCGGGTTAAG GGTGGTGGGG AGGGGGGGCA
TACGGATTCC 60
AATCTGGCTA GGTCGGGTTG TGGTAAGGTG GCCAGGACCA GCAGGCTTCA
GCATATCAAC 120
CCGCGCGCTA CCCCCCCTC CCGGTCTAGA ATCGAAGGTC 160

(2) INFORMATION FOR SEQ ID NO: 90:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:
TCTCACTCCT CGAGTTGGAC TCGGTGGGGC AAGCACANTC ATGGGGGGTT
TGTGAACAAG 60
TCTCCCCCTG GGAAGAACGC CACGAGCCCC TACACCGACG CCCAGCTGCC
CAGTGATCAG 120
GGTCCTCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 91:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:
TCTCACTCCT CGAGTCAGGT TGATTCGTTT CGTAATAGCT TTCGGTGGTA
TGAGCCGAGC 60
AGGGCTCTGT GCCATGGTTG TGGTAAGCGC GACACCTCCA CCACTCGTAT
CCACAATAGC 120
CCCAGCGACT CCTATCCTAC ACGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 92:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
 TCTCACTCCT CGAGCTTTT GCGGTTCCAG AGTCCGAGGT TCGAGGATTA
 CAGTAGGACG 60
 ATCTNTCGGT TGC GCAACGC CACGAACCCG AGTAATGTCT CCGATGCGCA
 CAATAACCGG 120
 GCCTTGGCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:
 TCTCACTCCT CGAGGAGCAT CACCGACGGG GGCATCAATG AGGTGGACCT
 GAGTAGTGTG 60
 TCGAACGTTC TTGAGAACGC CAACTCGCAT AGGGCCTACA GGAAGCATCG
 CCCGACCTTG 120
 AAGCGTCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:
 TCTCACTCCT CGAGTTCGAA GGTGAGCAGC CCGAGGGATC CGACGGTCCC
 GCGGAAGGGC 60
 GGCAATGTTG ATTATGGTTG TGGTCACAGG TCTTCCGCCC GGATGCCTAC
 CTCCGCTCTG 120
 TCGTCGATCA CGAAGTGCTA CACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
 177

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
 TCTCACTCCT CGAGAGCCAG TANGCAGGGC GGCCGGGGTG TTGCCCTGA
 GTTTGGGGCG 60

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Patent No. 7,053,177

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AGCGTTTTGG GTNGTGGTTG TGGTAGCGCC ACTTATTACA CGAACTCCAC
CAGCTGCAAG 120
GATGCTATGG GCCACAATA CTCGTCTAGA ATCGAAGGTC GCGNTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

TCTCACTCCT CGAGATGGTG CGAGAAGCAC AAGTTTACGG CTGCGCGTTG
CAGCGCGGGG 60
GCGGGTTTTG AGAGGGANGC CAGCCGTCCG CCCCAGCCTG CCCACCGGGA
TAATACCAAC 120
CGTAATGCNT NTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCTCACTCCT CGAGTTTCA GGTGTACCCG GACCATGGTC TGGAGAGGCA
TGCTTTGGAC 60
GGGACGGGTC CGCTTTACGC CATGCCCCGGC CGCTGGATTA GGGCGCGTCC
GCAGAACAGG 120
GACCGCCAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCTCACTCCT CGAGCAGGTG TACGGACAAC GAGCAGTGCC CCGATACCGG
GANTAGGTCT 60
CGTTCCGTTA GTAACGCCAG GTACTTTTCG AGCAGGTTGC TCAAGACTCA
CGCCCCCAT 120
CGCCCTTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

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(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TCTCACTCCT CGAGTGCCAG GGATAGCGGG CCTGCGGAGG ATGGGTCCCC
CGCCGTCCGG 60

TTGAACGGGG TTGAGAACGC CAACACTAGG AAGTCCTCCC GCAGTAACCC
GCGGGGTAGG 120

CGCCATCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TCTCACTCCT CGAGTTCCGC CGATGCGGAG AAGTGTGCGG GCAGTCTGTT
GTGGTGGGGT 60

AGGCAGAACA ACTCCGTTG TGGTTCGCCC ACGAAGAAGC ATCTGAAGCA
CCGCAATCGC 120

AGTCAGACCT CCTCTTCGTC CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TCTCACTCCT CGAGACCGAA GAACGTGGCC GATGCTTATT CGTCTCAGGA
CGGGGCGGCG 60

GCCGAGGAGA CGTCTCACGC CAGTAATGCC GCGCGGAAGT CCCCTAAGCA
CAAGCCCTTG 120

AGGCGGCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

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Patent No. 7,053,177

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(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:
TCTCACTCCT CGAGAGGCAG TACGGGGACG GCCGGCGGCG AGCGTTCCGG
GGTGCTCAAC 60
CTGCACACCA GGGATAACGC CAGCGGCAGC GGTTTCAAAC CGTGGTACCC
TTCGAATCGG 120
GGTCACAAGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 103:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:
TCTCACTCCT CGAGGTGGGG GTGGGAGAGG AGTCCGTCCG ACTACGATTC
TGATATGGAC 60
TTGGGGGCGA GGAGGTACGC CACCCGCACC CACCGCGCGC CCCCTCGCGT
CTTGAAGGCT 120
CCCCTGCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 104:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:
TCTCACTCCT CGAGGCACTG GAAGTGCAGG GGCTCTCAGG CTGCCTACGG
GGACAAGGAT 60
ATCGGGAGGT CCAGGGGTTG TGGTTCATT ACAAAGAATA AACTAATCA
CGCCCATCCT 120
AGCCACGGCG CCGTTGCTAA GATCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:
TCTCACTCCT CGAGCCGCGA GGAGGCGAAC TGGGACGGCT ATAAGAGGGA
GATGAGCCAC 60
CGGAGTCGCT TTTGGGACGC CACCCACCTG TCCCGCCCTC GCCGCCCCGC
TAACTCTGGT 120
GACCCTAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TCTCACTCNT CGAGAGAGTT CGCGGAGAGG AGGTTGTGGG GGTGTGATGA
CCTGAGTTGG 60
CGTCTCGACG CGGAGGGTTG TGGTCCCACT CCGAGCAATC GGGCCGTCAA
GCATCGCAAG 120
CCCCGCCCAC GCTCCCCCGC ACTCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TCTCACTCNT NGAGTGATCA CGCGTTGGGG ACGAATCTGA GGTCTGACAA
TGCCAAGGAG 60
CCGGGTGATT ACAACTGTTG TGGTAACGGG AACTCTACCG GGCGAAAGGT
TTTTAACCGT 120
AGGCGCCCCT CCGCCATCCC CANTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
177

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
 TCTCACTCCT CGAGGCATAT TTCTGAGTAT AGCTTTGCGA ATTCCCACTT
 GATGGGTGGC 60
 GAGTCCAAGC GGAAGGGTTG TGGTATTAAC GGCTCCTTTT CTCCCACTTG
 TCCCCGCTCC 120
 CCCACCCCAG CCTTCCGCCG CACCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA
 177

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TCTCACTCCT CGAGCCGGGA GAGCGGGATG TGGGGTAGTT GGTGGCGTGG
 TCACAGGTTG 60
 AATTCCACGG GGGGTAACGC CAACATGAAT GCTAGTCTGC CCCCCGACCC
 CCCTGTTTCC 120
 ACTCCGTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAG 158

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
 1 5 10 15
 Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
 20 25 30
 Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
 35 40 45
 Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
 50 55 60
 Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
 65 70 75 80
 Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
 85 90 95
 Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
 100 105 110
 Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
 115 120 125

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Patent No. 7,053,177

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Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
 130 135 140
 Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
 145 150 155 160
 Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
 165 170 175
 Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His
 180 185 190
 Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
 195 200 205
 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
 210 215 220
 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
 225 230 235 240
 Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
 245 250 255
 Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
 260 265 270
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
 275 280 285
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
 290 295 300
 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
 305 310 315 320
 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
 325 330 335
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
 340 345 350
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
 355 360 365
 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
 370 375 380
 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu
 385 390 395 400
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val
 405 410 415
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val
 420 425 430
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr
 435 440 445
 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val
 450 455 460
 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys
 465 470 475 480
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu
 485 490 495

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Patent No. 7,053,177

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Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser
 500 505 510
 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe
 515 520 525
 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn
 530 535 540
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg
 545 550 555 560
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala
 565 570 575
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr
 580 585 590
 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser
 595 600 605
 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu
 610 615 620
 Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly
 625 630 635 640
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu
 645 650 655
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr
 660 665 670
 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys
 675 680 685
 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser
 690 695 700
 Gln Lys Gln Met
 705

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

TCCGGACTCT CATAAGCGCC GG

22

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
ACAACGGGCC AGAAAGAGCG AG 22

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
ACACCACCCC AATCGGAGCT AC 22

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:
TCAGAATCCG TGCACTGGCC AA 22

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:
GCCCTATTCA TACCACCGGA GT 22

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:
CATCAGTCCT ACCGCCGAAA AG 22

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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Patent No. 7,053,177

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
CGTATAGCTA TTGTGAGCGA TG 22

(2) INFORMATION FOR SEQ ID NO: 118:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:
ACGCGCGGAA CGAGCAGTAC CA 22

(2) INFORMATION FOR SEQ ID NO: 119:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:
CCATAATGAT CCCCCTCACT AT 22

(2) INFORMATION FOR SEQ ID NO: 120:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:
AGACACCCCT TAGCCGTCGT AG 22

(2) INFORMATION FOR SEQ ID NO: 121:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:
AGCTCCGTGA CCTTAGTCAT AA 22

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Patent No. 7,053,177

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGCACAGCTC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGGGTCATC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGTCACCCCC CTCCCCGGAC TT 22

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ACTCGCAATT ATTGGCGCTC GA 22

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
GTCTTCTCAA CCTTATCCTG CG 22

(2) INFORMATION FOR SEQ ID NO: 127:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:
AAAGCCCCCT GCTAAACTCC CA 22

(2) INFORMATION FOR SEQ ID NO: 128:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:
CTGCGTCTGC CACGTCGTCA TC 22

(2) INFORMATION FOR SEQ ID NO: 129:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:
GTTAAAAGAG GGCAAGCTCG GA 22

(2) INFORMATION FOR SEQ ID NO: 130:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:
CCGAGTTCTT GATGTCCTCC AT 22

(2) INFORMATION FOR SEQ ID NO: 131:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:
TCCAATGCCT GTACCACGGA TG 22

(2) INFORMATION FOR SEQ ID NO: 132:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:
TCGCAACCGA TATCGTGCTT AT 22

(2) INFORMATION FOR SEQ ID NO: 133:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:
TGCATACACT GCTTGGAGCC CT 22

(2) INFORMATION FOR SEQ ID NO: 134:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:
GAAATCTCAC TAGTAGTCCG CC 22

(2) INFORMATION FOR SEQ ID NO: 135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:
GCGGGCAAGA CAGTCCAATT CC 22

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
GAGCTCCAAT TCCACGACGA CC 22

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:
GGTTGCCATG CGTTCAAAC AC 22

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:
TCCCGCGGGG ACAAACCCGA AT 22

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:
CTGCTAGTCT TATCATTCCC CA 22

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:
CTATCGACAC TATAGGGCCT AC 22

(2) INFORMATION FOR SEQ ID NO: 141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:
TACCCTTGTA ACCCACTA GG 22

(2) INFORMATION FOR SEQ ID NO: 142:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:
TTCTTCTGAA TAGACCGGCC GA 22

(2) INFORMATION FOR SEQ ID NO: 143:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:
CCACCACCCT TAACCCGACA AT 22

(2) INFORMATION FOR SEQ ID NO: 144:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:
AGGGGGAGAC TTGTTCAAA AC 22

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(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CGGCTCATAC CACCGAAAGC TA

22

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ATCGTCCTAC TGTAATCCTC GA

22

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GACACACTAC TCAGGTCCAC CT

22

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

CCATAATCAA CATTGCCGCC CT

22

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
CAAAACGCTC GCCCCAAACT CA 22

(2) INFORMATION FOR SEQ ID NO: 150:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:
GTAAACTTGT GCTTCTCGCA CC 22

(2) INFORMATION FOR SEQ ID NO: 151:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:
CCATGGTCCG GGTACACCTG AA 22

(2) INFORMATION FOR SEQ ID NO: 152:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:
GTTACTAACG GAACGAGACC TA 22

(2) INFORMATION FOR SEQ ID NO: 153:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:
TGTGCGGTT CTCAACCCCG TT 22

(2) INFORMATION FOR SEQ ID NO: 154:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:
ACAACCGGAG TTGTTCTGCC TA

22

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:
TAAGCATCGG CCACGTTCTT CG

22

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:
TTATCCCTGG TGTGCAGGTT GA

22

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:
TATCAGAATC GTAGTCGGAC GG

22

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:
CTTTGTAATG GAACCACAAC CC 22

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:
CGGTGGCTCA TCTCCCTCTT AT 22

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
ATCAGACTGG CTGGGACCAC AA 22

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
CACAACTCC TCTCCGCGAA CT 22

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:
AGATTCGTCC CCAACGCGTG AT 22

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

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Patent No. 7,053,177

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:
 GGGAATTCGC AAAGCTATAC TC 22

(2) INFORMATION FOR SEQ ID NO: 164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:
 CCCC GTGGAA TTCAACCTGT GA 22

(2) INFORMATION FOR SEQ ID NO: 165:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:
 GTCGTCTTTC CAGACGT 17

(2) INFORMATION FOR SEQ ID NO: 166:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
 CTTGCATGCC TGCAGGTCGA C 21

(2) INFORMATION FOR SEQ ID NO: 167:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
 Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala Phe Glu

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Patent No. 7,053,177

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1 5 10 15
 Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln Leu Ser
 20 25 30
 Phe Thr Pro Glu Glu
 35

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp
 1 5 10 15
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val
 20 25 30
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe
 1 5 10 15
 Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro
 20 25 30
 Thr Pro Gln Leu Pro Arg Gly Pro Asn
 35 40

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
 1 5 10 15

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Patent No. 7,053,177

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Ser Asp Ser Asp
20

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
1 5 10 15
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn
20 25

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Thr Asn Ala Lys His Ser Ser His Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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Patent No. 7,053,177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile
 1 5 10 15

Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly
 20 25 30

Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp
 35 40 45

Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr
 50 55 60

Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys
 65 70 75 80

Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala
 85 90 95

Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp
 100 105 110

Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly
 115 120 125

Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser
 130 135 140

Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn
 145 150 155 160

Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu
 165 170 175

Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His

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Patent No. 7,053,177

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180 185 190
 Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu
 195 200 205
 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys
 210 215 220
 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile
 225 230 235 240
 Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro
 245 250 255
 Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg
 260 265 270
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile
 275 280 285
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp
 290 295 300
 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile
 305 310 315 320
 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met
 325 330 335
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly
 340 345 350
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala
 355 360 365
 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys
 370 375 380
 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu
 385 390 395 400
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val
 405 410 415
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val
 420 425 430
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr
 435 440 445
 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val
 450 455 460
 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys
 465 470 475 480
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu
 485 490 495
 Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser
 500 505 510
 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe
 515 520 525
 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn
 530 535 540
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg

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545 550 555 560
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala
 565 570 575
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr
 580 585 590
 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser
 595 600 605
 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu
 610 615 620
 Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly
 625 630 635 640
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu
 645 650 655
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr
 660 665 670
 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys
 675 680 685
 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser
 690 695 700
 Gln Lys Gln Met
 705

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 88...2583
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

GAATTCCGTC TCGACCACTG AATGGAAGAA AAGGACTTTT AACCACCATT
 TTGTGACTTA 60
 CAGAAAGGAA TTTGAATAAA GAAAACT ATG ATA CTT CAG GCC CAT CTT CAC TCC
 114

Met Ile Leu Gln Ala His Leu His Ser

1 5

CTG TGT CTT CTT ATG CTT TAT TTG GCA ACT GGA TAT GGC CAA GAG GGG 162

Leu Cys Leu Leu Met Leu Tyr Leu Ala Thr Gly Tyr Gly Gln Glu Gly

10 15 20 25

AAG TTT AGT GGA CCC CTG AAA CCC ATG ACA TTT TCT ATT TAT GAA GGC 210

Lys Phe Ser Gly Pro Leu Lys Pro Met Thr Phe Ser Ile Tyr Glu Gly

30 35 40

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CAA GAA CCG AGT CAA ATT ATA TTC CAG TTT AAG GCC AAT CCT CCT GCT	258
Gln Glu Pro Ser Gln Ile Ile Phe Gln Phe Lys Ala Asn Pro Pro Ala	
45 50 55	
GTG ACT TTT GAA CTA ACT GGG GAG ACA GAC AAC ATA TTT GTG ATA GAA	306
Val Thr Phe Glu Leu Thr Gly Glu Thr Asp Asn Ile Phe Val Ile Glu	
60 65 70	
CGG GAG GGA CTT CTG TAT TAC AAC AGA GCC TTG GAC AGG GAA ACA AGA	354
Arg Glu Gly Leu Leu Tyr Tyr Asn Arg Ala Leu Asp Arg Glu Thr Arg	
75 80 85	
TCT ACT CAC AAT CTC CAG GTT GCA GCC CTG GAC GCT AAT GGA ATT ATA	402
Ser Thr His Asn Leu Gln Val Ala Ala Leu Asp Ala Asn Gly Ile Ile	
90 95 100 105	
GTG GAG GGT CCA GTC CCT ATC ACC ATA GAA GTG AAG GAC ATC AAC GAC	450
Val Glu Gly Pro Val Pro Ile Thr Ile Glu Val Lys Asp Ile Asn Asp	
110 115 120	
AAT CGA CCC ACG TTT CTC CAG TCA AAG TAC GAA GGC TCA GTA AGG CAG	498
Asn Arg Pro Thr Phe Leu Gln Ser Lys Tyr Glu Gly Ser Val Arg Gln	
125 130 135	
AAC TCT CGC CCA GGA AAG CCC TTC TTG TAT GTC AAT GCC ACA GAC CTG	546
Asn Ser Arg Pro Gly Lys Pro Phe Leu Tyr Val Asn Ala Thr Asp Leu	
140 145 150	
GAT GAT CCG GCC ACT CCC AAT GGC CAG CTT TAT TAC CAG ATT GTC ATC	594
Asp Asp Pro Ala Thr Pro Asn Gly Gln Leu Tyr Tyr Gln Ile Val Ile	
155 160 165	
CAG CTT CCC ATG ATC AAC AAT GTC ATG TAC TTT CAG ATC AAC AAC AAA	642
Gln Leu Pro Met Ile Asn Asn Val Met Tyr Phe Gln Ile Asn Asn Lys	
170 175 180 185	
ACG GGA GCC ATC TCT CTT ACC CGA GAG GGA TCT CAG GAA TTG AAT CCT	690
Thr Gly Ala Ile Ser Leu Thr Arg Glu Gly Ser Gln Glu Leu Asn Pro	
190 195 200	
GCT AAG AAT CCT TCC TAT AAT CTG GTG ATC TCA GTG AAG GAC ATG GGA	738
Ala Lys Asn Pro Ser Tyr Asn Leu Val Ile Ser Val Lys Asp Met Gly	
205 210 215	
GGC CAG AGT GAG AAT TCC TTC AGT GAT ACC ACA TCT GTG GAT ATC ATA	786
Gly Gln Ser Glu Asn Ser Phe Ser Asp Thr Thr Ser Val Asp Ile Ile	
220 225 230	
GTG ACA GAG AAT ATT TGG AAA GCA CCA AAA CCT GTG GAG ATG GTG GAA	834
Val Thr Glu Asn Ile Trp Lys Ala Pro Lys Pro Val Glu Met Val Glu	
235 240 245	
AAC TCA ACT GAT CCT CAC CCC ATC AAA ATC ACT CAG GTG CGG TGG AAT	882
Asn Ser Thr Asp Pro His Pro Ile Lys Ile Thr Gln Val Arg Trp Asn	
250 255 260 265	
GAT CCC GGT GCA CAA TAT TCC TTA GTT GAC AAA GAG AAG CTG CCA AGA	930
Asp Pro Gly Ala Gln Tyr Ser Leu Val Asp Lys Glu Lys Leu Pro Arg	
270 275 280	
TTC CCA TTT TCA ATT GAC CAG GAA GGA GAT ATT TAC GTG ACT CAG CCC	978

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Phe Pro Phe Ser Ile Asp Gln Glu Gly Asp Ile Tyr Val Thr Gln Pro
 285 290 295
 TTG GAC CGA GAA GAA AAG GAT GCA TAT GTT TTT TAT GCA GTT GCA AAG 1026
 Leu Asp Arg Glu Glu Lys Asp Ala Tyr Val Phe Tyr Ala Val Ala Lys
 300 305 310
 GAT GAG TAC GGA AAA CCA CTT TCA TAT CCG CTG GAA ATT CAT GTA AAA 1074
 Asp Glu Tyr Gly Lys Pro Leu Ser Tyr Pro Leu Glu Ile His Val Lys
 315 320 325
 GTT AAA GAT ATT AAT GAT AAT CCA CCT ACA TGT CCG TCA CCA GTA ACC 1122
 Val Lys Asp Ile Asn Asp Asn Pro Pro Thr Cys Pro Ser Pro Val Thr
 330 335 340 345
 GTA TTT GAG GTC CAG GAG AAT GAA CGA CTG GGT AAC AGT ATC GGG ACC 1170
 Val Phe Glu Val Gln Glu Asn Glu Arg Leu Gly Asn Ser Ile Gly Thr
 350 355 360
 CTT ACT GCA CAT GAC AGG GAT GAA GAA AAT ACT GCC AAC AGT TTT CTA 1218
 Leu Thr Ala His Asp Arg Asp Glu Glu Asn Thr Ala Asn Ser Phe Leu
 365 370 375
 AAC TAC AGG ATT GTG GAG CAA ACT CCC AAA CTT CCC ATG GAT GGA CTC 1266
 Asn Tyr Arg Ile Val Glu Gln Thr Pro Lys Leu Pro Met Asp Gly Leu
 380 385 390
 TTC CTA ATC CAA ACC TAT GCT GGA ATG TTA CAG TTA GCT AAA CAG TCC 1314
 Phe Leu Ile Gln Thr Tyr Ala Gly Met Leu Gln Leu Ala Lys Gln Ser
 395 400 405
 TTG AAG AAG CAA GAT ACT CCT CAG TAC AAC TTA ACG ATA GAG GTG TCT 1362
 Leu Lys Lys Gln Asp Thr Pro Gln Tyr Asn Leu Thr Ile Glu Val Ser
 410 415 420 425
 GAC AAA GAT TTC AAG ACC CTT TGT TTT GTG CAA ATC AAC GTT ATT GAT 1410
 Asp Lys Asp Phe Lys Thr Leu Cys Phe Val Gln Ile Asn Val Ile Asp
 430 435 440
 ATC AAT GAT CAG ATC CCC ATC TTT GAA AAA TCA GAT TAT GGA AAC CTG 1458
 Ile Asn Asp Gln Ile Pro Ile Phe Glu Lys Ser Asp Tyr Gly Asn Leu
 445 450 455
 ACT CTT GCT GAA GAC ACA AAC ATT GGG TCC ACC ATC TTA ACC ATC CAG 1506
 Thr Leu Ala Glu Asp Thr Asn Ile Gly Ser Thr Ile Leu Thr Ile Gln
 460 465 470
 GCC ACT GAT GCT GAT GAG CCA TTT ACT GGG AGT TCT AAA ATT CTG TAT 1554
 Ala Thr Asp Ala Asp Glu Pro Phe Thr Gly Ser Ser Lys Ile Leu Tyr
 475 480 485
 CAT ATC ATA AAG GGA GAC AGT GAG GGA CGC CTG GGG GTT GAC ACA GAT 1602
 His Ile Ile Lys Gly Asp Ser Glu Gly Arg Leu Gly Val Asp Thr Asp
 490 495 500 505
 CCC CAT ACC AAC ACC GGA TAT GTC ATA ATT AAA AAG CCT CTT GAT TTT 1650
 Pro His Thr Asn Thr Gly Tyr Val Ile Ile Lys Lys Pro Leu Asp Phe
 510 515 520
 GAA ACA GCA GCT GTT TCC AAC ATT GTG TTC AAA GCA GAA AAT CCT GAG 1698
 Glu Thr Ala Ala Val Ser Asn Ile Val Phe Lys Ala Glu Asn Pro Glu

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525 530 535
 CCT CTA GTG TTT GGT GTG AAG TAC AAT GCA AGT TCT TTT GCC AAG TTC 1746
 Pro Leu Val Phe Gly Val Lys Tyr Asn Ala Ser Ser Phe Ala Lys Phe
 540 545 550
 ACG CTT ATT GTG ACA GAT GTG AAT GAA GCA CCT CAA TTT TCC CAA CAC 1794
 Thr Leu Ile Val Thr Asp Val Asn Glu Ala Pro Gln Phe Ser Gln His
 555 560 565
 GTA TTC CAA GCG AAA GTC AGT GAG GAT GTA GCT ATA GGC ACT AAA GTG 1842
 Val Phe Gln Ala Lys Val Ser Glu Asp Val Ala Ile Gly Thr Lys Val
 570 575 580 585
 GGC AAT GTG ACT GCC AAG GAT CCA GAA GGT CTG GAC ATA AGC TAT TCA 1890
 Gly Asn Val Thr Ala Lys Asp Pro Glu Gly Leu Asp Ile Ser Tyr Ser
 590 595 600
 CTG AGG GGA GAC ACA AGA GGT TGG CTT AAA ATT GAC CAC GTG ACT GGT 1938
 Leu Arg Gly Asp Thr Arg Gly Trp Leu Lys Ile Asp His Val Thr Gly
 605 610 615
 GAG ATC TTT AGT GTG GCT CCA TTG GAC AGA GAA GCC GGA AGT CCA TAT 1986
 Glu Ile Phe Ser Val Ala Pro Leu Asp Arg Glu Ala Gly Ser Pro Tyr
 620 625 630
 CGG GTA CAA GTG GTG GCC ACA GAA GTA GGG GGG TCT TCC TTA AGC TCT 2034
 Arg Val Gln Val Val Ala Thr Glu Val Gly Gly Ser Ser Leu Ser Ser
 635 640 645
 GTG TCA GAG TTC CAC CTG ATC CTT ATG GAT GTG AAT GAC AAC CCT CCC 2082
 Val Ser Glu Phe His Leu Ile Leu Met Asp Val Asn Asp Asn Pro Pro
 650 655 660 665
 AGG CTA GCC AAG GAC TAC ACG GGC TTG TTC TTC TGC CAT CCC CTC AGT 2130
 Arg Leu Ala Lys Asp Tyr Thr Gly Leu Phe Phe Cys His Pro Leu Ser
 670 675 680
 GCA CCT GGA AGT CTC ATT TTC GAG GCT ACT GAT GAT GAT CAG CAC TTA 2178
 Ala Pro Gly Ser Leu Ile Phe Glu Ala Thr Asp Asp Asp Gln His Leu
 685 690 695
 TTT CGG GGT CCC CAT TTT ACA TTT TCC CTC GGC AGT GGA AGC TTA CAA 2226
 Phe Arg Gly Pro His Phe Thr Phe Ser Leu Gly Ser Gly Ser Leu Gln
 700 705 710
 AAC GAC TGG GAA GTT TCC AAA ATC AAT GGT ACT CAT GCC CGA CTG TCT 2274
 Asn Asp Trp Glu Val Ser Lys Ile Asn Gly Thr His Ala Arg Leu Ser
 715 720 725
 ACC AGG CAC ACA GAC TTT GAG GAG AGG GCG TAT GTC GTC TTG ATC CGC 2322
 Thr Arg His Thr Asp Phe Glu Glu Arg Ala Tyr Val Val Leu Ile Arg
 730 735 740 745
 ATC AAT GAT GGG GGT CGG CCA CCC TTG GAA GGC ATT GTT TCT TTA CCA 2370
 Ile Asn Asp Gly Gly Arg Pro Pro Leu Glu Gly Ile Val Ser Leu Pro
 750 755 760
 GTT ACA TTC TGC AGT TGT GTG GAA GGA AGT TGT TTC CGG CCA GCA GGT 2418
 Val Thr Phe Cys Ser Cys Val Glu Gly Ser Cys Phe Arg Pro Ala Gly
 765 770 775

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CAC CAG ACT GGG ATA CCC ACT GTG GGC ATG GCA GTT GGT ATA CTG CTG 2466
His Gln Thr Gly Ile Pro Thr Val Gly Met Ala Val Gly Ile Leu Leu
780 785 790
ACC ACC CTT CTG GTG ATT GGT ATA ATT TTA GCA GTT GTG TTT ATC CGC 2514
Thr Thr Leu Leu Val Ile Gly Ile Ile Leu Ala Val Val Phe Ile Arg
795 800 805
ATA AAG AAG GAT AAA GGC AAA GAT AAT GTT GAA AGT GCT CAA GCA TCT 2562
Ile Lys Lys Asp Lys Gly Lys Asp Asn Val Glu Ser Ala Gln Ala Ser
810 815 820 825
GAA GTC AAA CCT CTG AGA AGC TGAATTTGAA AAGGAATGTT TGAATTTATA TAGC
2617
Glu Val Lys Pro Leu Arg Ser
830
AAGTGCTATT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAACG
TGCATTATAA 2677
TTTTTTAAAC AGATATTCCC TCTTGTCCTT TAATATTTGC TAAATATTTT TTTTTTGAGG
2737
TGGAGTCTTG CTCTGTCGCC CAGGCTGGAG TACAGTGGTG TGATCCCAGC
TCACTGCAAC 2797
CTCCGCCTCC TGGGTTTACA TGATTCTCCT GCCTCAGCTT CCTAAGTAGC
TGGGTTTACA 2857
GGCACCCACC ACCATGCCCA GCTAATTTTT GTATTTTAA TAGAGACGGG
GTTTCGCCAT 2917
TTGGCCAGGC TGGTCTTGAA CTCCTGACGT CAAGTGATCT GCCTGCCTTG
GTCTCCCAAT 2977
ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTTCA TGTGCTATAG
ACATTAGAGA 3037
GATTTTTCAT TTTTCCATGA CATTTTTCCT CTCTGCAAAT GGCTTAGCTA CTTGTGTTTT
3097
TCCCTTTTGG GGCAAGACAG ACTCATTAAT TATTCTGTAC ATTTTTTCTT
TATCAAGGAG 3157
ATATATCAGT GTTGTCTCAT AGAACTGCCT GGATTCCATT TATGTTTTTT CTGATTCCAT
3217
CCTGTGTCCC CTTATCCTT GACTCCTTTG GTATTTCACT GAATTTCAAA CATTTGTCAG
3277
AGAAGAAAAA AGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC
TTTTGCGGCC 3337
GCGAATTC 3345

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr
 1 5 10 15
 Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys
 20 25 30
 Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile
 35 40 45
 Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly
 50 55 60
 Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr
 65 70 75 80
 Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val
 85 90 95
 Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile
 100 105 110
 Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln
 115 120 125
 Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro
 130 135 140
 Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn
 145 150 155 160
 Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn
 165 170 175
 Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr
 180 185 190
 Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn
 195 200 205
 Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe
 210 215 220
 Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys
 225 230 235 240
 Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro
 245 250 255
 Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser
 260 265 270
 Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln
 275 280 285
 Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp
 290 295 300
 Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu
 305 310 315 320
 Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn
 325 330 335
 Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn
 340 345 350
 Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp

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355 360 365
 Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln
 370 375 380
 Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala
 385 390 395 400
 Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro
 405 410 415
 Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu
 420 425 430
 Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile
 435 440 445
 Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn
 450 455 460
 Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro
 465 470 475 480
 Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser
 485 490 495
 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr
 500 505 510
 Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn
 515 520 525
 Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys
 530 535 540
 Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val
 545 550 555 560
 Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser
 565 570 575
 Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp
 580 585 590
 Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly
 595 600 605
 Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro
 610 615 620
 Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr
 625 630 635 640
 Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile
 645 650 655
 Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr
 660 665 670
 Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe
 675 680 685
 Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr
 690 695 700
 Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys
 705 710 715 720
 Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Asp Phe Glu

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      725      730      735
Glu Arg Ala Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro
      740      745      750
Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val
      755      760      765
Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr
      770      775      780
Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly
      785      790      795      800
Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys
      805      810      815
Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser
      820      825      830

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1827 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

Met Ala Arg Lys Lys Phe Ser Gly Leu Glu Ile Ser Leu Ile Val Leu
 1       5       10      15
Phe Val Ile Val Thr Ile Ile Ala Ile Ala Leu Ile Val Val Leu Ala
 20      25      30
Thr Lys Thr Pro Ala Val Asp Glu Ile Ser Asp Ser Thr Ser Thr Pro
 35      40      45
Ala Thr Thr Arg Val Thr Thr Asn Pro Ser Asp Ser Gly Lys Cys Pro
 50      55      60
Asn Val Leu Asn Asp Pro Val Asn Val Arg Ile Asn Cys Ile Pro Glu
 65      70      75      80
Gln Phe Pro Thr Glu Gly Ile Cys Ala Gln Arg Gly Cys Cys Trp Arg
 85      90      95
Pro Trp Asn Asp Ser Leu Ile Pro Trp Cys Phe Phe Val Asp Asn His
100      105     110
Gly Tyr Asn Val Gln Asp Met Thr Thr Thr Ser Ile Gly Val Glu Ala
115      120     125
Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn
130      135     140
Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe
145      150     155     160
Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr
165      170     175
Val Lys Glu Phe Thr Gly Pro Thr Val Ser Asp Thr Leu Tyr Asp Val
180      185     190

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Lys Val Ala Gln Asn Pro Phe Ser Ile Gln Val Ile Arg Lys Ser Asn
 195 200 205
 Gly Lys Thr Leu Phe Asp Thr Ser Ile Gly Pro Leu Val Tyr Ser Asp
 210 215 220
 Gln Tyr Leu Gln Ile Ser Ala Arg Leu Pro Ser Asp Tyr Ile Tyr Gly
 225 230 235 240
 Ile Gly Glu Gln Val His Lys Arg Phe Arg His Asp Leu Ser Trp Lys
 245 250 255
 Thr Trp Pro Ile Phe Thr Arg Asp Gln Leu Pro Gly Asp Asn Asn Asn
 260 265 270
 Asn Leu Tyr Gly His Gln Thr Phe Phe Met Cys Ile Glu Asp Thr Ser
 275 280 285
 Gly Lys Ser Phe Gly Val Phe Leu Met Asn Ser Asn Ala Met Glu Ile
 290 295 300
 Phe Ile Gln Pro Thr Pro Ile Val Thr Tyr Arg Val Thr Gly Gly Ile
 305 310 315 320
 Leu Asp Phe Tyr Ile Leu Leu Gly Asp Thr Pro Glu Gln Val Val Gln
 325 330 335
 Gln Tyr Gln Gln Leu Val Gly Leu Pro Ala Met Pro Ala Tyr Trp Asn
 340 345 350
 Leu Gly Phe Gln Leu Ser Arg Trp Asn Tyr Lys Ser Leu Asp Val Val
 355 360 365
 Lys Glu Val Val Arg Arg Asn Arg Glu Ala Gly Ile Pro Phe Asp Thr
 370 375 380
 Gln Val Thr Asp Ile Asp Tyr Met Glu Asp Lys Lys Asp Phe Thr Tyr
 385 390 395 400
 Asp Gln Val Ala Phe Asn Gly Leu Pro Gln Phe Val Gln Asp Leu His
 405 410 415
 Asp His Gly Gln Lys Tyr Val Ile Ile Leu Asp Pro Ala Ile Ser Ile
 420 425 430
 Gly Arg Arg Ala Asn Gly Thr Thr Tyr Ala Thr Tyr Glu Arg Gly Asn
 435 440 445
 Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile
 450 455 460
 Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro
 465 470 475 480
 Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu
 485 490 495
 Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe
 500 505 510
 Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro
 515 520 525
 Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile
 530 535 540
 Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser
 545 550 555 560

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Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys
 565 570 575
 Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala
 580 585 590
 Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser
 595 600 605
 Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu
 610 615 620
 Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu
 625 630 635 640
 Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr
 645 650 655
 Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro
 660 665 670
 Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr
 675 680 685
 Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr
 690 695 700
 Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu
 705 710 715 720
 Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp
 725 730 735
 Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr
 740 745 750
 Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly
 755 760 765
 Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala
 770 775 780
 Asp Lys Ile Gly Leu His Leu Arg Gly Gly Tyr Ile Ile Pro Ile Gln
 785 790 795 800
 Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu
 805 810 815
 Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp
 820 825 830
 Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu
 835 840 845
 Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His
 850 855 860
 Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile
 865 870 875 880
 Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn
 885 890 895
 Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln
 900 905 910
 Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser
 915 920 925

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Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr
 930 935 940
 Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys
 945 950 955 960
 Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe
 965 970 975
 Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser
 980 985 990
 Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile
 995 1000 1005
 Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys Tyr
 1010 1015 1020
 His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln Lys Lys
 1025 1030 1035 1040
 Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr Pro Ile Ser
 1045 1050 1055
 Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys Glu Asn Pro Phe
 1060 1065 1070
 Gly Ile Gln Ile Arg Arg Arg Ser Ser Gly Arg Val Ile Trp Asp Ser
 1075 1080 1085
 Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln Phe Ile Gln Ile Ser Thr
 1090 1095 1100
 Arg Leu Pro Ser Glu Tyr Ile Tyr Gly Phe Gly Glu Val Glu His Thr
 1105 1110 1115 1120
 Ala Phe Lys Arg Asp Leu Asn Trp Asn Thr Trp Gly Met Phe Thr Arg
 1125 1130 1135
 Asp Gln Pro Pro Gly Tyr Lys Leu Asn Ser Tyr Gly Phe His Pro Tyr
 1140 1145 1150
 Tyr Met Ala Leu Glu Glu Glu Gly Asn Ala His Gly Val Phe Leu Leu
 1155 1160 1165
 Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr
 1170 1175 1180
 Tyr Arg Thr Val Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro
 1185 1190 1195 1200
 Thr Pro Gln Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro
 1205 1210 1215
 Val Met Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly
 1220 1225 1230
 Tyr Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala
 1235 1240 1245
 Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met Glu
 1250 1255 1260
 Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu Pro Gln
 1265 1270 1275 1280
 Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile Ile Ile Leu
 1285 1290 1295

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Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr Pro Ala Phe Glu
 1300 1305 1310
 Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp Pro Asn Thr Asn Asp
 1315 1320 1325
 Ile Cys Trp Ala Lys Val Trp Pro Asp Leu Pro Asn Ile Thr Ile Asp
 1330 1335 1340
 Lys Thr Leu Thr Glu Asp Glu Ala Val Asn Ala Ser Arg Ala His Val
 1345 1350 1355 1360
 Ala Phe Pro Asp Phe Phe Arg Thr Ser Thr Ala Glu Trp Trp Ala Arg
 1365 1370 1375
 Glu Ile Val Asp Phe Tyr Asn Glu Lys Met Lys Phe Asp Gly Leu Trp
 1380 1385 1390
 Ile Asp Met Asn Glu Pro Ser Ser Phe Val Asn Gly Thr Thr Thr Asn
 1395 1400 1405
 Gln Cys Arg Asn Asp Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu
 1410 1415 1420
 Thr Lys Arg Thr Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala
 1425 1430 1435 1440
 Glu Gln Ile Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His
 1445 1450 1455
 Asn Leu Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln
 1460 1465 1470
 Lys Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro
 1475 1480 1485
 Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala Arg
 1490 1495 1500
 Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe Ser Leu
 1505 1510 1515 1520
 Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe Phe Asn Asn
 1525 1530 1535
 Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu Gly Ala Phe Tyr
 1540 1545 1550
 Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr Arg Arg Gln Asp Pro
 1555 1560 1565
 Ala Ser Trp Asn Glu Thr Phe Ala Glu Met Ser Arg Asn Ile Leu Asn
 1570 1575 1580
 Ile Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Gln Met His Glu Ile
 1585 1590 1595 1600
 His Ala Asn Gly Gly Thr Val Ile Arg Pro Leu Leu His Glu Phe Phe
 1605 1610 1615
 Asp Glu Lys Pro Thr Trp Asp Ile Phe Lys Gln Phe Leu Trp Gly Pro
 1620 1625 1630
 Ala Phe Met Val Thr Pro Val Leu Glu Pro Tyr Val Gln Thr Val Asn
 1635 1640 1645
 Ala Tyr Val Pro Asn Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp
 1650 1655 1660

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Ile Gly Val Arg Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr
 1665 1670 1675 1680
 Ile Asn Leu His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro
 1685 1690 1695
 Ala Gln Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val
 1700 1705 1710
 Ala Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp
 1715 1720 1725
 Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val Gln
 1730 1735 1740
 Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys Arg Gly
 1745 1750 1755 1760
 Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His Val Trp Gly
 1765 1770 1775
 Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr Tyr Asn Gly Asn
 1780 1785 1790
 Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr Asn Met Ile Leu Arg
 1795 1800 1805
 Ile Asp Leu Thr Thr His Asn Val Thr Leu Glu Glu Pro Ile Glu Ile
 1810 1815 1820
 Asn Trp Ser
 1825

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 45...2099
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GCCTTACTGC AGGAAGGCAC TCCGAAGACA TAAGTCGGTG AGAC ATG GCT GAA GAT
56

Met Ala Glu Asp

1

AAA AGC AAG AGA GAC TCC ATC GAG ATG AGT ATG AAG GGA TGC CAG ACA 104
Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys Gly Cys Gln Thr

5 10 15 20
AAC AAC GGG TTT GTC CAT AAT GAA GAC ATT CTG GAG CAG ACC CCG GAT 152
Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu Gln Thr Pro Asp

25 30 35
CCA GGC AGC TCA ACA GAC AAC CTG AAG CAC AGC ACC AGG GGC ATC CTT 200

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Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr Arg Gly Ile Leu
 40 45 50
 GGC TCC CAG GAG CCC GAC TTC AAG GGC GTC CAG CCC TAT GCG GGG ATG 248
 Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro Tyr Ala Gly Met
 55 60 65
 CCC AAG GAG GTG CTG TTC CAG TTC TCT GGC CAG GCC CGC TAC CGC ATA 296
 Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala Arg Tyr Arg Ile
 70 75 80
 CCT CGG GAG ATC CTC TTC TGG CTC ACA GTG GCT TCT GTG CTG GTG CTC 344
 Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser Val Leu Val Leu
 85 90 95 100
 ATC GCG GCC ACC ATA GCC ATC ATT GCC CTC TCT CCA AAG TGC CTA GAC 392
 Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro Lys Cys Leu Asp
 105 110 115
 TGG TGG CAG GAG GGG CCC ATG TAC CAG ATC TAC CCA AGG TCT TTC AAG 440
 Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro Arg Ser Phe Lys
 120 125 130
 GAC AGT AAC AAG GAT GGG AAC GGA GAT CTG AAA GGT ATT CAA GAT AAA 488
 Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly Ile Gln Asp Lys
 135 140 145
 CTG GAC TAC ATC ACA GCT TTA AAT ATA AAA ACT GTT TGG ATT ACT TCA 536
 Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val Trp Ile Thr Ser
 150 155 160
 TTT TAT AAA TCG TCC CTT AAA GAT TTC AGA TAT GGT GTT GAA GAT TTC 584
 Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly Val Glu Asp Phe
 165 170 175 180
 CGG GAA GTT GAT CCC ATT TTT GGA ACG ATG GAA GAT TTT GAG AAT CTG 632
 Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp Phe Glu Asn Leu
 185 190 195
 GTT GCA GCC ATA CAT GAT AAA GGT TTA AAA TTA ATC ATC GAT TTC ATA 680
 Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile Ile Asp Phe Ile
 200 205 210
 CCA AAC CAC ACG AGT GAT AAA CAT ATT TGG TTT CAA TTG AGT CGG ACA 728
 Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln Leu Ser Arg Thr
 215 220 225
 CGG ACA GGA AAA TAT ACT GAT TAT TAT ATC TGG CAT GAC TGT ACC CAT 776
 Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His Asp Cys Thr His
 230 235 240
 GAA AAT GGC AAA ACC ATT CCA CCC AAC AAC TGG TTA AGT GTG TAT GGA 824
 Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu Ser Val Tyr Gly
 245 250 255 260
 AAC TCC AGT TGG CAC TTT GAC GAA GTG CGA AAC CAA TGT TAT TTT CAT 872
 Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln Cys Tyr Phe His
 265 270 275
 CAG TTT ATG AAA GAG CAA CCT GAT TTA AAT TTC CGC AAT CCT GAT GTT 920
 Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg Asn Pro Asp Val

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      280      285      290
CAA GAA GAA ATA AAA GAA ATT TTA CGG TTC TGG CTC ACA AAG GGT GTT   968
Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu Thr Lys Gly Val
      295      300      305
GAT GGT TTT AGT TTG GAT GCT GTT AAA TTC CTC CTA GAA GCA AAG CAC   1016
Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu Glu Ala Lys His
      310      315      320
CTG AGA GAT GAG ATC CAA GTA AAT AAG ACC CAA ATC CCG GAC ACG GTC   1064
Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile Pro Asp Thr Val
      325      330      335      340
ACA CAA TAC TCG GAG CTG TAC CAT GAC TTC ACC ACC ACG CAG GTG GGA   1112
Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr Thr Gln Val Gly
      345      350      355
ATG CAC GAC ATT GTC CGC AGC TTC CGG CAG ACC ATG GAC CAA TAC AGC   1160
Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met Asp Gln Tyr Ser
      360      365      370
ACG GAG CCC GGC AGA TAC AGG TTC ATG GGG ACT GAA GCC TAT GCA GAG   1208
Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu Ala Tyr Ala Glu
      375      380      385
AGT ATT GAC AGG ACC GTG ATG TAC TAT GGA TTG CCA TTT ATC CAA GAA   1256
Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro Phe Ile Gln Glu
      390      395      400
GCT GAT TTT CCC TTC AAC AAT TAC CTC AGC ATG CTA GAC ACT GTT TCT   1304
Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu Asp Thr Val Ser
      405      410      415      420
GGG AAC AGC GTG TAT GAG GTT ATC ACA TCC TGG ATG GAA AAC ATG CCA   1352
Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met Glu Asn Met Pro
      425      430      435
GAA GGA AAA TGG CCT AAC TGG ATG ATT GGT GGA CCA GAC AGT TCA CGG   1400
Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro Asp Ser Ser Arg
      440      445      450
CTG ACT TCG CGT TTG GGG AAT CAG TAT GTC AAC GTG ATG AAC ATG CTT   1448
Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val Met Asn Met Leu
      455      460      465
CTT TTC ACA CTC CCT GGA ACT CCT ATA ACT TAC TAT GGA GAA GAA ATT   1496
Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr Gly Glu Glu Ile
      470      475      480
GGA ATG GGA AAT ATT GTA GCC GCA AAT CTC AAT GAA AGC TAT GAT ATT   1544
Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu Ser Tyr Asp Ile
      485      490      495      500
AAT ACC CTT CGC TCA AAG TCA CCA ATG CAG TGG GAC AAT AGT TCA AAT   1592
Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp Asn Ser Ser Asn
      505      510      515
GCT GGT TTT TCT GAA GCT AGT AAC ACC TGG TTA CCT ACC AAT TCA GAT   1640
Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro Thr Asn Ser Asp
      520      525      530

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TAC CAC ACT GTG AAT GTT GAT GTC CAA AAG ACT CAG CCC AGA TCG GCT 1688
 Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln Pro Arg Ser Ala
 535 540 545
 TTG AAG TTA TAT CAA GAT TTA AGT CTA CTT CAT GCC AAT GAG CTA CTC 1736
 Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala Asn Glu Leu Leu
 550 555 560
 CTC AAC AGG GGC TGG TTT TGC CAT TTG AGG AAT GAC AGC CAC TAT GTT 1784
 Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp Ser His Tyr Val
 565 570 575 580
 GTG TAC ACA AGA GAG CTG GAT GGC ATC GAC AGA ATC TTT ATC GTG GTT 1832
 Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile Phe Ile Val Val
 585 590 595
 CTG AAT TTT GGA GAA TCA ACA CTG TTA AAT CTA CAT AAT ATG ATT TCG 1880
 Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His Asn Met Ile Ser
 600 605 610
 GGC CTT CCC GCT AAA ATA AGA ATA AGG TTA AGT ACC AAT TCT GCC GAC 1928
 Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr Asn Ser Ala Asp
 615 620 625
 AAA GGC AGT AAA GTT GAT ACA AGT GGC ATT TTT CTG GAC AAG GGA GAG 1976
 Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu Asp Lys Gly Glu
 630 635 640
 GGA CTC ATC TTT GAA CAC AAC ACG AAG AAT CTC CTT CAT CGC CAA ACA 2024
 Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu His Arg Gln Thr
 645 650 655 660
 GCT TTC AGA GAT AGA TGC TTT GTT TCC AAT CGA GCA TGC TAT TCC AGT 2072
 Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala Cys Tyr Ser Ser
 665 670 675
 GTA CTG AAC ATA CTG TAT ACC TCG TGT TAGGCACCTT TATGAAGAGA TGAAGAC
 2126
 Val Leu Asn Ile Leu Tyr Thr Ser Cys
 680 685
 ACTGGCATT T CAGTGGGATT GTAAGCATT GTAATAGCTT CATGTACAGC
 ATGCTGCTT 2186
 GTGAACAATC ATTAATTCTT CGATATTCT GTAGCTTGAA TGTAACCGCT
 TTAAGAAAGG 2246
 TTCTCAAATG TTTTGAAAAA AATAAAATGT TTAAAAGT 2284

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys

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1      5      10      15
Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu
20      25      30
Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr
35      40      45
Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro
50      55      60
Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala
65      70      75      80
Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser
85      90      95
Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro
100     105     110
Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro
115     120     125
Arg Ser Phe Lys Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly
130     135     140
Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val
145     150     155     160
Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly
165     170     175
Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp
180     185     190
Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile
195     200     205
Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln
210     215     220
Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His
225     230     235     240
Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu
245     250     255
Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln
260     265     270
Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg
275     280     285
Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu
290     295     300
Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu
305     310     315     320
Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile
325     330     335
Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr
340     345     350
Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met
355     360     365
Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu

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      370      375      380
Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro
385      390      395      400
Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu
      405      410      415
Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met
      420      425      430
Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro
      435      440      445
Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val
      450      455      460
Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr
      465      470      475      480
Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu
      485      490      495
Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp
      500      505      510
Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro
      515      520      525
Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln
      530      535      540
Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala
      545      550      555      560
Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp
      565      570      575
Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile
      580      585      590
Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His
      595      600      605
Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr
      610      615      620
Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu
      625      630      635      640
Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu
      645      650      655
His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala
      660      665      670
Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys
      675      680      685

```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Leu Val Pro Arg Gly Ser Pro Gly Ile Pro Gly Ser Arg Val Gly Gln
1 5 10 15
Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His
20 25 30
Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg
35 40 45
Pro Leu Arg Gln Ala Ser
50

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
1 5 10 15
Leu Asn Gly

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Asp Gly Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr
1 5 10 15
Arg Lys Ser Ser Arg
20

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg
1 5 10 15

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Arg His Pro

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Ser Arg Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His
1 5 10 15
Ser Ser His Asn Arg
20

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser
1 5 10 15
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

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Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser
 1 5 10 15
 Ser Ser Val Arg Gly Gly Cys Gly
 20

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly
 1 5 10 15
 Cys Gly Ala His Ser Ser Pro Pro Arg Ala
 20 25

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr
 1 5 10 15
 Met Val Ser Arg Leu
 20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Lys Lys Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala
 1 5 10 15
 Phe Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln
 20 25 30
 Leu Ser Phe Thr Pro Glu Glu
 35

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Asn Ala Lys His Ser Ser His Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:
 Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:
 Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:
 Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg
 1 5 10 15
 Ser Cys Ala

(2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala
 1 5 10 15
 Gly Thr Arg Asn Ser
 20

(2) INFORMATION FOR SEQ ID NO: 201:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala

1 5 10 15

Ser Gln His

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp

1 5 10 15

Ser Asp Ser Asp Thr Met Ala Lys His Ser Ser His Asn Arg Arg Leu

20 25 30

Arg Thr Arg Ser Arg Pro Asn Gly

35 40

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Tyr Ser Lys Val

1

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Phe Pro His Leu

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1

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Tyr Arg Gly Val

1

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Tyr Gln Thr Ile

1

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Thr Glu Gln Phe

1

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Thr Glu Val Met

1

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(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Thr Ser Ala Phe

1

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Tyr Thr Arg Phe

1

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...714
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC 48

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1 5 10 15

ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG 96

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

20 25 30

TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG 144

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu

35 40 45

GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA 192

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

50 55 60

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TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC   240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA   288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT   336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110
AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA   384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115     120     125
ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT   432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130     135     140
GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT   480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145     150     155     160
GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA   528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165     170     175
GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC   576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180     185     190
TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC   624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195     200     205
ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT   672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210     215     220
GGA TCC CCA GGA ATT CCC GGG TCG ACT CGA GCG GCC GCA TCG TGA   717
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser
225     230     235

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
20     25     30

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu

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```

      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
    100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
    115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
    145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
    165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
    180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
    195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Gln
    225      230      235      240
Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr Val Gly
    245      250      255
Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr Pro Ala
    260      265      270
Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
    275      280

```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
  20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
  35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
  50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
  65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
  85      90      95

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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asp
 225 230 235 240
 His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly
 245 250 255
 Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe
 260 265 270
 Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 275 280

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser

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      100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Pro
      225      230      235      240
Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe Gly Gly
      245      250      255
Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala Ser Leu
      260      265      270
Glu Pro Pro Ser Ser Asp Tyr
      275

```

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110

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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Gly
 225 230 235 240
 Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn Leu His
 245 250 255
 Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr Pro Ser
 260 265 270
 Asn Arg Gly His Lys
 275

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

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      115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
      225      230      235      240
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
      245      250      255
Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu
      260      265      270
Pro Arg Gly Pro Asn
      275

```

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
      50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
      65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
      100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115     120     125

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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
 225 230 235 240
 Ser Gly Gly Met Asn Arg Ala Tyr
 245

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu

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      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
      225      230      235      240
Val Phe Arg Glu Leu Arg Asp Arg
      245

```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
      50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
      65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
      100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115     120     125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130     135     140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
      145     150     155     160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165     170     175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180     185     190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195     200     205

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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn
 225 230 235 240
 Ala Thr Ser His His Thr Arg Pro
 245

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Pro
 225 230 235 240
 Gln Leu Pro Arg Gly Pro Asn

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245

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
 225 230 235 240
 Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
 245 250 255
 Arg Pro

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Gly Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn
 225 230 235 240
 Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro
 245 250 255
 Asn

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1         5         10        15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20        25        30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35        40        45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50        55        60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65        70        75        80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85        90        95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100       105       110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115       120       125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130       135       140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145       150       155       160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165       170       175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180       185       190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195       200       205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210       215       220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp
225       230       235       240
Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
245       250       255
Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
260       265

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

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```

1       5       10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100     105     110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115     120     125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130     135     140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145     150     155     160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165     170     175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180     185     190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195     200     205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210     215     220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His
225     230     235     240
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg
245     250     255
Asp Arg Trp Asn Ala Thr Ser Ala Ala Thr Arg Pro Thr Pro Gln Leu
260     265     270
Pro Arg Gly Pro Asn
275

```

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1       5       10      15

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser Ala
 225 230 235 240
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
 245 250 255
 Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg
 260 265 270
 Gly Arg Arg His Pro
 275

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

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20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala
 225 230 235 240
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn
 245 250 255
 Gly

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

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50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Asp Gly
 225 230 235 240
 Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys
 245 250 255
 Ser Ser Arg

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu

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85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
 225 230 235 240
 Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
 245 250 255
 Pro

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

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115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn
 225 230 235 240
 Ala Asn Thr Arg Lys Ser Ser Arg
 245

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Arg Lys
 225 230 235 240
 Ser Ser Arg Ser Asn Pro Arg Gly
 245

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala

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195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Asn
 225 230 235 240
 Pro Arg Gly Arg Arg His Pro
 245

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Arg
 225 230 235 240

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Lys Ser Ser Arg Ser Asn Pro Arg Gly
245

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
225 230 235 240
Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
245 250 255
Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
260 265 270
Arg Ser Arg Pro Asn

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275

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr
 225 230 235 240
 Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp
 245 250 255
 Ser Asp

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Arg
 225 230 235 240
 Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser
 245 250 255
 His Asn Arg

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn
 225 230 235 240
 Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro
 245 250 255
 Asn

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Thr Asn
 225 230 235 240
 Ala Lys His Ser Ser His Asn
 245

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: <Unknown>
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys

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50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ser
 225 230 235 240
 His Asn Arg Arg Leu Arg Thr Arg
 245

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Arg
 225 230 235 240
 Leu Arg Thr Arg Ser Arg Pro Asn
 245

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn

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130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255
 Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile
 260 265 270
 Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 275 280

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val
 225 230 235 240
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 245 250 255
 Ala

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Val Arg
 225 230 235 240
 Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr
 245 250 255
 Arg Asn Ser

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Thr
 225 230 235 240
 Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Gln
 245 250 255
 His

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
 225 230 235 240

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Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser
 245 250 255
 Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg
 260 265 270
 Gly Pro Arg Gly Thr Met Val Ser Arg Leu
 275 280

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
 225 230 235 240
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser

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245 250 255
Val Arg Gly Gly Cys Gly
260

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Cys
225 230 235 240
Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly Cys Gly
245 250 255
Ala His Ser Ser Pro Pro Arg Ala
260

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(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Ala
 225 230 235 240
 His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr Met Val
 245 250 255
 Ser Arg Leu

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:
 Ser Gly Ser Pro Pro Cys Cys Cys Ser Trp Gly Arg Phe Met Gln Gly
 1 5 10 15
 Gly Leu Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg
 20 25 30
 Thr Ser Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu
 1 5 10 15
 Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro
 20 25 30
 Gln Leu Pro Arg Gly Pro Asn Ser
 35 40

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15
 Ser Arg Pro Asn Gly
 20

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: <Unknown>
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu
1 5 10 15
Arg Gln Ala Ser Ala His Gly
20

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

(B) LOCATION: 1

(D) OTHER INFORMATION: "Xaa=Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

(B) LOCATION: 2

(D) OTHER INFORMATION: "Xaa=Ser, Ala or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Asp Xaa Asp Xaa Arg Arg Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Site

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(B) LOCATION: 7

(D) OTHER INFORMATION: "Xaa=Ala or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser

1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asp Ser Asp Val Arg Arg Pro Trp

1 5

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Ala Asp Gln Arg Arg Gly Trp

1 5

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Asp Gly Arg Gly Gly Arg Ser Tyr

1 5

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Val Arg Ser

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1

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 2...2

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Cys Xaa Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys
 1 5 10 15
 Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val
 20 25 30
 Ser Leu Ser Lys Gln
 35

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

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Patent No. 7,053,177

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Ac-Cys
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:
Xaa Leu Asn Gly Gly Val Lys Met Tyr Val Glu Ser Val Asp Arg Tyr
1 5 10 15
Val Cys

(2) INFORMATION FOR SEQ ID NO: 268:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Ac-Cys
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:
Xaa Leu Asn Gly Gly Val Lys Phe Ile Thr Cys Met Tyr Val Glu Ser
1 5 10 15
Val Asp Arg Tyr Val Cys
20

(2) INFORMATION FOR SEQ ID NO: 269:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 2...2
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:
Cys Xaa Arg Leu Asn Gly Gly Val Ser Met Tyr Val Glu Ser Val Asp
1 5 10 15
Arg Tyr Val Cys Arg
20

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(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val
 1 5 10 15
 Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser
 20 25 30
 Asn Pro Arg Gly Arg Arg His Pro
 35 40

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Xaa Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp
 1 5 10 15
 Gly Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu
 20 25 30
 Lys His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Xaa Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser
1 5 10 15
Trp Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala
20 25 30
Val Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Xaa Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe
1 5 10 15
Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro
20 25 30
Thr Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Xaa Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val
1 5 10 15
Phe Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg

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Patent No. 7,053,177

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20 25 30
Pro Thr Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
1 5 10 15
Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
20 25 30
Pro Gln Leu Pro Arg Gly Pro Asn
35 40

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Xaa Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg
1 5 10 15
Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr
20 25 30
Pro Gln Leu Pro Arg Gly Pro Asn Ser
35 40

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

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Patent No. 7,053,177

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(C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:
 Xaa Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu
 1 5 10 15
 Thr Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala
 20 25 30
 Thr Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 278:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:
 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
 Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His
 20 25 30
 Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 279:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

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Xaa Ser Gly Ser Gly Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg
 1 5 10 15
 Arg Pro Trp Ala Arg Ser Cys Ala
 20

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
 Arg Ser Cys Ala
 20

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Xaa Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val
 1 5 10 15
 Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
 20 25 30
 Leu Arg Thr Arg Ser Arg Pro Asn Gly
 35 40

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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Patent No. 7,053,177

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:
Xaa Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu
1 5 10 15
Asn Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp
 20 25 30
Tyr Pro Ser Asn Arg Gly His Lys
 35 40

(2) INFORMATION FOR SEQ ID NO: 283:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:
Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala
 20

(2) INFORMATION FOR SEQ ID NO: 284:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=biotin-Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:
Xaa Ser Gly Ser Gly Leu Tyr Ala Asn Pro Gly Met Tyr Ser Arg Leu
1 5 10 15
His Ser Pro Ala

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20

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
 1 5 10 15
 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
 20 25 30
 Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

Xaa Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu
 1 5 10 15
 Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser
 20 25 30
 Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Xaa Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys

1 5 10 15

Ser Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg

20 25 30

Ala Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu

35 40 45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

Xaa Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val

1 5 10 15

Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser

20 25 30

Asn Pro Arg Gly Arg Arg His Pro Gly Gly

35 40

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

Xaa Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly

1 5 10 15

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Trp Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp
 20 25 30
 Tyr Asn Gln Leu Pro Ser Asp Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Xaa Ser Glu Ala Asn Leu Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
 1 5 10 15
 Arg Arg Asn Ser Ser Thr Arg Pro Arg Thr Ser Pro Asn Ser Val His
 20 25 30
 Ala Arg Tyr Pro Ser Thr Asp His Asp
 35 40

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified Base

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=biotin-S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Xaa Gly Ser Gly Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro
 1 5 10 15
 Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His
 20 25 30
 Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn Gly
 35 40

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:
 Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
 1 5 10 15
 Arg Ser Cys Ala His Gln Gly
 20

(2) INFORMATION FOR SEQ ID NO: 293:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:
 Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
 1 5 10 15
 Leu Arg Gln Ala Ser Ala His Gly
 20

(2) INFORMATION FOR SEQ ID NO: 294:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:
 Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
 1 5 10 15
 Arg Arg His Pro Gly

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20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
1 5 10 15

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Gly

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15
 Ser Arg Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

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Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Xaa Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly
 1 5 10 15
 Ala Gly Thr Arg Asn Ser
 20

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Xaa Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

Xaa Ser Arg Ala Asn Thr Asp Gly Arg Lys Ser Arg Tyr Ser Ser Pro
 1 5 10 15
 Arg Arg Asn Ser Ser Thr Glu Pro Arg Leu Ser Pro Asn Ser Val His
 20 25 30
 Ala Arg Tyr Pro Ser Thr Asp His Asp
 35 40

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Xaa Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:
Xaa Ser Asn Pro Arg Gly Arg Arg His Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 307:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:
Xaa Glu Asn Ala Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 308:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:
Xaa Ala Asn Thr Arg Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 309:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other

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(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:
Xaa Thr Arg Lys Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 310:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:
Xaa Arg Lys Ser Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:
Xaa Lys Ser Ser Arg Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 312:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:
Xaa Ser Ser Arg Ser Asn Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Xaa Arg Ser Asn Pro Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Xaa Ser Asn Pro Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Xaa Pro Arg Gly Arg Arg His

1

5

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Xaa Arg Arg His Pro Gly

1

5

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Xaa Lys Ser Ser Arg Gly Asn

1

5

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

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Xaa Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Xaa Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:
Xaa Thr Asn Ala Lys His Ser Ser His Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:
Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:
Xaa Arg Arg Leu Arg Thr Arg Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

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Xaa Arg Arg Leu Arg Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Xaa Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys
 1 5 10 15
 Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
 20 25

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
 1 5 10 15
 Glu Pro Gly Cys
 20

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Xaa Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:
Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Xaa Arg Lys Val Phe Asn Arg Arg Arg Pro Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Xaa Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Xaa Asn Arg Arg Arg Pro Ser

1 5

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp

1 5 10 15

Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu

20 25 30

Arg Thr Arg Ser Arg Pro Asn Gly

35 40

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu

1 5 10 15

Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys

20 25 30

Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr

35 40

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys

1 5 10 15
Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Xaa Asn Leu Arg Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys

1 5 10 15
Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys Val Phe Asn Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg

1 5 10 15
Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:
 Xaa Ala Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 340:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:
 Xaa Ser Ala His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 341:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:
 Xaa Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 342:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:
 Xaa Ser Ser His Ala Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 343:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:
 Xaa Ser Ser His Asn Ala Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 344:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 Xaa Ser Ser His Asn Arg Ala Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 345:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Xaa Ser Ser His Asn Arg Arg Ala Arg Thr Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Xaa Ser Ser His Asn Arg Arg Leu Ala Thr Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Xaa Ser Ser His Asn Arg Arg Leu Arg Ala Arg

1 5 10

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:
 Xaa Ser Ser His Asn Arg Arg Leu Arg Thr Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 349:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:
 Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 350:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:
 Xaa Gly Arg Asn His Asp Val Val Ser Ser Asn Thr His Lys Ser Tyr
 1 5 10 15
 Arg Ser Pro Arg Ser Ala Ser Tyr Pro Arg Leu Ser Asn Asp Arg Thr
 20 25 30
 Asp Arg Thr Glu Pro Ala Pro Ser Ser
 35 40

(2) INFORMATION FOR SEQ ID NO: 351:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: Other

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Xaa Arg Asn Thr Arg Asn Lys Thr Ser Arg Leu Ser Ala Asn Pro His

1 5 10 15

Arg Ser His Arg

20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 20...20

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser

1 5 10 15

Arg Pro Asn Xaa

20

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 10...10

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Arg Arg Leu Arg Thr Arg Ser Arg Lys Xaa

1 5 10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15
Glu Pro Gly Asp Tyr
20

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Xaa Ser Asp Asn Ala Lys Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn
1 5 10 15
Gly Asn Ser Thr Gly
20

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Xaa Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:
Xaa Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:
Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:
Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MEMORY
 (B) STRAIN: DISPLAY MEMORY
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:
 Xaa Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 361:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:
 Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
 1 5 10 15
 Pro Gly

(2) INFORMATION FOR SEQ ID NO: 362:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:
 Xaa Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His
 1 5 10 15
 Pro Gly

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(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
 1 5 10 15
 Arg

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Cys Arg Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Xaa Thr Asn Ala Lys His Ser Ser Cys Asn Arg Arg Leu Arg Cys Arg
 1 5 10 15

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(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Xaa Ala Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Xaa Thr Ala Ala Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

Xaa Thr Asn Gly Lys Asn Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 369:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Xaa Thr Asn Ala Lys Ala Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Xaa Thr Asn Ala Lys His Ala Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Xaa Thr Asn Ala Lys His Ser Ala His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:
Xaa Thr Asn Ala Lys His Ser Ser Ala Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 373:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:
Xaa Thr Asn Ala Lys His Ser Ser His Ala Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 374:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Ala Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 375:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Ala Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Ala Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Ala Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:
Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr
 1 5 10 15
 Arg

(2) INFORMATION FOR SEQ ID NO: 382:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:
 Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 383:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:
 Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 384:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

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- (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:
 Xaa Lys Ser Ser His Asn Arg Arg Leu Arg Thr Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 385:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 386:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:
 Xaa Lys Thr Asn Ala Lys His Ser Ser His Asn Arg
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 387:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Xaa Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Xaa Ala Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Xaa Pro Ala Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Xaa Pro Gly Ala Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Xaa Pro Gly Asp Ala Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Xaa Pro Gly Asp Tyr Ala Cys Cys Gly Asn Gly Asn Ser Thr Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:
Xaa Pro Gly Asp Tyr Asn Ala Cys Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:
Xaa Pro Gly Asp Tyr Asn Cys Ala Gly Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:
Xaa Pro Gly Asp Tyr Asn Cys Cys Ala Asn Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: Other

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(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Ala Gly Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Ala Asn Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Ala Ser Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

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(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ala Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Xaa Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Pro Gly Asp Tyr Asn Cys Gly Asn Cys Asn Ser Thr Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg
 1 5 10 15

Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn
 20 25 30

Pro Arg Gly Arg Arg His Pro Gly
 35 40

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala
 1 5 10 15

Ser Ala His

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: <Unknown>

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:
Xaa Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala
1 5 10 15
Arg Ser Cys Ala His
20

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xaa=Lys(dns)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Xaa Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro
1 5 10 15
Leu Arg Gln Ala Ser Ala His
20

MAILING ADDRESS OF SENDER

Patent No. 7,053,177

MORGAN, LEWIS & BOCKIUS LLP
1111 Pennsylvania Avenue, NW
Washington, DC 20004